

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: March 2, 2003, 07:42:38 ; Search time 1893 Seconds

(without alignments)
3766.607 Million cell updates/sec

Title: US-09-744-502-20

Perfect score: 245
Sequence: 1 ttagaggggaataaaagtc.....tgaacgcatcataaact 245Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pal:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
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26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rtd:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	245	100.0	675	8 RSP242875	AJ242875 Rhizocton
2	238.6	97.4	652	8 RSP242879	AJ242879 Rhizocton
3	235.4	96.1	661	8 RSP242880	AJ242880 Rhizocton
4	234.6	95.8	668	8 RSP242877	AJ242877 Rhizocton
5	231.6	94.5	654	8 RSP242878	AJ242878 Rhizocton
6	231.2	94.4	657	8 RSP242876	AJ242876 Rhizocton
7	229.8	93.8	660	8 RSP242885	AJ242885 Rhizocton
8	225.6	92.1	661	8 RSP242886	AJ242886 Rhizocton
9	216.4	88.3	665	8 RSP242881	AJ242881 Rhizocton
10	174	71.0	659	8 RSP242897	AJ242897 Rhizocton
11	166.2	67.8	661	8 RSP242898	AJ242898 Rhizocton
12	166.2	67.8	661	8 RSP242899	AJ242899 Rhizocton
13	144	58.8	661	8 RSP242892	AJ242892 Rhizocton
14	142.6	58.2	664	8 RSP242902	AJ242902 Rhizocton
15	140.8	57.5	661	8 RSP242893	AJ242893 Rhizocton
16	137.2	56.0	626	8 AF461605	AF461605 Unculture
17	135.6	55.3	647	8 RSP242883	AJ242883 Rhizocton
18	133.6	54.5	698	8 RSP242903	AJ242903 Rhizocton
19	122	49.8	635	8 RSP242884	AJ242884 Rhizocton
20	117.2	47.8	655	8 RSP242894	AJ242894 Rhizocton
21	117.2	47.8	656	8 RSP242895	AJ242895 Rhizocton
22	114.8	46.9	641	8 RSP242882	AJ242882 Rhizocton
23	112	45.7	669	8 RSP242887	AJ242887 Rhizocton
24	111.6	45.6	1491	8 AF354094	AF354094 Ceratobas
25	108.2	44.2	649	8 RSP242890	AJ242890 Rhizocton
26	108.2	44.2	656	8 RSP242896	AJ242896 Rhizocton
27	106.6	43.5	649	8 RSP242891	AJ242891 Rhizocton
28	106.6	43.5	854	8 AF200518	AF200518 Rhizocton
29	106.6	43.5	854	8 AF200519	AF200519 Rhizocton
30	104.8	42.8	701	8 RSP242900	AJ242900 Ceratobas
31	104.6	42.7	589	8 CCO301900	AJ301900 Ceratobas
32	103.2	42.1	605	8 FU419931	AJ419931 Rhizocton
33	100.6	41.1	591	8 RSU19963	U19963 Rhizoctonia
34	98.2	40.1	692	8 RSP242901	AJ242901 Rhizocton
35	97.6	39.8	1477	8 AF354093	AF354093 Ceratobas
36	96.4	39.3	590	8 CCO302006	AJ302006 Ceratobas
37	96	39.2	860	8 AF200516	AF200516 Rhizocton
38	96	39.2	860	8 AF200517	AF200517 Rhizocton
39	95.6	39.0	590	8 RSU19962	U19962 Rhizoctonia
40	94.4	38.5	591	8 CCO301899	AJ301899 Ceratobas
41	94.4	38.5	594	8 CCO301903	AJ301903 Ceratobas
42	92.8	37.9	576	8 CCO301902	AJ301902 Ceratobas
43	87.4	35.7	578	8 AF502772	AF502772 Leaf lilt
44	86.4	35.3	850	8 AF200520	AF200520 Rhizocton
45	86.2	35.2	585	8 CCO301901	AJ301901 Ceratobas

ALIGNMENTS

RESULT 1
RSP242875 675 bp DNA linear PLN 15-JAN-2002
LOCUS Rhizoctonia sp. Eab-F1 5.8S rRNA gene and ITS1 and 2, strain
DEFINITION Eab-F1.
ACCESSION AJ242875
VERSION AJ242875.1 GI:18181597
KEYWORDS 5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer 1;
internal transcribed spacer 2; ITS1; ITS2.
SOURCE Rhizoctonia sp. Eab-F1.
ORGANISM Rhizoctonia sp. Eab-F1
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Heterobasidiomycetidae; Ceratobasidiaceae;
Ceratobasidiaceae; Ceratobasidiaceae; Rhizoctonia.

REFERENCE
1

Pred. No. is the number of results predicted by chance to have a

FEATURES	source
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 675)
AUTHORS	Julian M.C.
TITLE	Direct Submission
JOURNAL	Submitted (02-JUN-1999) Julian M.C., Departamento de Biotecnologia Microbiana, Centro Nacional de Biotecnologia, Campus Cantoblanco, Universidad Autonoma de Madrid, Madrid 28049, SPAIN
LOCATION/Qualifiers	
1. .675	/organism="Rhizoctonia sp. Eab-F1"
/strain="Eab-F1"	
/db_xref="taxon:183679"	
/country="Spain"	
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/gene="5.8S rRNA"	
/product="5.8S ribosomal RNA"	
401. .>675	
misc-feature	/note="internal transcribed spacer 2, (ITS2)"
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Best Local Similarity	100.0% Pred. No. 8.5e-57;
Matches 245: Conservative	0; Mismatches 0; Indels 0; Gaps 0
1	TTAGAGGGGAAATAAAAGTCTGTAACAGGTTTCCGTAAGTGAACCTCGCGAAGATCATTT
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61	ATTGATGATGATTTAGAGTTGGTTGCGTGCCTCCTCGGAGACATGTGCACGCTTTC
61	ATTGATGATGATTTAGAGTTGGTTGCGTGCCTCCTCGGAGACATGTGCACGCTTTC
121	TTTCATCCACACACACCTGTGCACCTGTGAGACGGAGACCGTAAAAAAGTCTCCGCTC
121	TTTCATCCACACACACCTGTGCACCTGTGAGACGGAGACCGTAAAAAAGTCTCCGCTC
181	ATTAACACCAACAACCCCATTTGTTAAATTTGAATGTAATGTAACCATCATTA
181	ATTAACACCAACAACCCCATTTGTTAAATTTGAATGTAATGTAACCATCATTA
241	AAACT 245
241	AAACT 245
RESULT 2	
LOCUS	RSP242879
DEFINITION	Rhizoctonia sp. Eab-F6 5.8S rRNA gene and ITS1 and 2, strain
ACCESSION	RSP242879
VERSION	AJ242879.1 GI:18181601
KEYWORDS	5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer 1; internal transcribed spacer 2; ITS1; ITS2.
SOURCE	Rhizoctonia sp. Eab-F6
ORGANISM	Rhizoctonia sp. Eab-F6
REFERENCE	Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
AUTHORS	Heterobasidiomycetes; Heterobasidiomycetidae; Ceratobasidiales;
TITLE	Ceratobasidiaceae; mitosporic Ceratobasidiaceae; Rhizoctonia.
1	Salazar O., Munoz R., Lopez-Corcoles H. and Rubio V.
1	Molecular characterization and pathogenicity of a new group of
1	isolates of binucleate Rhizoctonia spp. (Ceratobasidium spp.)
1	isolated in Spain

JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 652)
AUTHORS	Julian M.C.
TITLE	Direct Submission
JOURNAL	Submitted (02-JUN-1999) Julian M.C., Departamento de Biotecnologia Microbiana, Centro Nacional de Biotecnologia, Campus Cantoblanco, Universidad Autonoma de Madrid, Madrid 28049, SPAIN
FEATURES	Location/Qualifiers
source	1..652
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	/strain="Eab-F6"
	/db_xref="taxon:183683"
	/country="Spain"
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	/gene="5.8S rRNA"
misc_feature	/product="5.8S ribosomal RNA"
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Best Local Similarity	98.4%; Pred. No. 4.8e-55;
Matches 241; Conservative	0; Mismatches 4; Indels 0; Gaps 0
QY	1 TTAGAGGGGAATTAATAAGTCGTACAAAGCTTCCGTAGTGAACCTGCGGAGAGATCATTT 60
Db	2 TTAGAGGGGAAGTAAAAAGTCGTAAACAAGGTTTCCGTAGTGAACCTGCGGAGAGATCATTT 61
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Db	62 ATTGAATGAATTTAGAGTGTGTTGTCGTCGGCTCCCTCGGAGACATGTGCAGCGTTTCTC 121
QY	121 TTTTCATCCACACACACCTTGTGCACCTTGTGACGAGAGACCGTAAAAAAGTCTTCGCTCT 180
Db	122 TTTTCATCCACACACACCTTGTGCACCTTGTGACGAGAGACCGTAAAAAAGTCTTCGCTCT 181
QY	181 ATTTAAACCCACAAACCCCATTTGATTTTAATTGAATGTAATGATGTAACGCATCATTA 240
Db	182 ATTTAAACCCACAAACCCCATTTGATTTTAATTGAATGTAATGATGTAACGCATCATTA 241
QY	241 AAACCT 245
Db	242 GAACCT 246
RESULT 3	
RSP242880	661 bp DNA linear PLN 15-JAN-2007
LOCUS	RSP242880
DEFINITION	Rhizoctonia sp. Eab-F7 5.8S rRNA gene and ITS1 and 2, strain Eab-F7.
ACCESSION	AJ242880
VERSION	AJ242880.1 GI:18181602
KEYWORDS	5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer 1; internal transcribed spacer 2; ITS1; ITS2.
SOURCE	Rhizoctonia sp. Eab-F7.
ORGANISM	Rhizoctonia sp. Eab-F7
REFERENCE	Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes; Heterobasidiomycetidae; Ceratobasidiales; Ceratobasidiaceae; mitosporic Ceratobasidiaceae; Rhizoctonia.
AUTHORS	Salazar, O., Munoz, R., Lopez-Corcoles, H. and Rubio, V.
TITLE	Molecular characterization and pathogenicity of a new group of isolates of binucleate Rhizoctonia spp. (Ceratobasidium spp.) isolated in Spain
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 661)
AUTHORS	Julian M.C.
TITLE	Direct Submission

JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 652)
AUTHORS	Julian M.C.
TITLE	Direct Submission
JOURNAL	Submitted (02-JUN-1999) Julian M.C., Departamento de Biotecnologia Microbiana, Centro Nacional de Biotecnologia, Campus Cantoblanco, Universidad Autonoma de Madrid, Madrid 28049, SPAIN
FEATURES	Location/Qualifiers
source	1..652
	/organism="Rhizoctonia sp. Eab-F6"
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	/db_xref="taxon:183683"
	/country="Spain"
misc_feature	<1..246
gene	/note="Internal transcribed spacer 1, (ITS1)"
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rRNA	/gene="5.8S rRNA"
	247..401
misc_feature	/gene="5.8S rRNA"
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	/note="Internal transcribed spacer 2, (ITS2)"
BASE COUNT	190 a 126 c 138 g 198 t
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Query Match	97.4%; Score 238.6; DB 8; Length 652;
Best Local Similarity	98.4%; Pred. No. 4.8e-55;
Matches 241; Conservative	0; Mismatches 4; Indels 0; Gaps 0
QY	1 TTAGAGGGGAATTAATAAGTCGTACAAAGCTTCCGTAGGTGAACCTGCGGAGAGATCATTT 60
Db	2 TTAGAGGGGAAGTAAAAAGTCGTAAACAAGGTTTCCGTAGGTGAACCTGCGGAGAGATCATTT 61
QY	61 ATTGAATGAATTTAGAGTGTGTTGTCGCGGCGCTCCCTCGGAGACATGTGCAGCGCTTCTC 120
Db	62 ATTGAATGAATTAAGAGTGTGTTGTCGCGCTCCCTCGGAGACATGTGCAGCGCTTCTC 121
QY	121 TTTTCATCCACACACACCTTGCACCTTGTGACGAGAGACCGTAAAAAAGTCTTCGCTCT 180
Db	122 TTTTCATCCACACACACCTTGCACCTTGTGACGAGAGACCGTAAAAAAGTCTTCGCTCT 181
QY	181 ATTTAAACCCACAAACCCCATTTGATTTTAATTTGAATGATGATGAACGCATCATTA 240
Db	182 ATTTAAACCCACAAACCCCATTTGATTTTAATTTGAATGATGATGAACGCATCATTA 241
QY	241 AAACCT 245
Db	242 GAACCT 246
RESULT 3	
RSP242880	661 bp DNA linear PLN 15-JAN-2007
LOCUS	RSP242880
DEFINITION	Rhizoctonia sp. Eab-F7 5.8S rRNA gene and ITS1 and 2, strain Eab-F7.
ACCESSION	AJ242880
VERSION	AJ242880.1 GI:18181602
KEYWORDS	5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer 1; internal transcribed spacer 2; ITS1; ITS2.
SOURCE	Rhizoctonia sp. Eab-F7.
ORGANISM	Rhizoctonia sp. Eab-F7
REFERENCE	Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes; Heterobasidiomycetidae; Ceratobasidiales; Ceratobasidiaceae; mitosporic Ceratobasidiaceae; Rhizoctonia.
AUTHORS	Salazar, O., Munoz, R., Lopez-Corcoles, H. and Rubio, V.
TITLE	Molecular characterization and pathogenicity of a new group of isolates of binucleate Rhizoctonia spp. (Ceratobasidium spp.) isolated in Spain
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 661)
AUTHORS	Julian M.C.
TITLE	Direct Submission

	misc_feature	<1..238	/note="internal transcribed spacer 1, (ITS1)"
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	rRNA	239..393	/gene="5.8S rRNA"
	misc_feature	394..>654	/product="5.8S ribosomal RNA"
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Best Local Similarity	98.3%;	Pred. No. 4e-53;	
Matches 234; Conservative	0;	Mismatches 4;	Indels 0; Gaps 0;
Oy	8	GGATMAAAAGTCGTAAACAAGTTCCGTAGTGAACCTCGCGAAGAGATCATATTGAAT	67
Db	1	GGAACTMAAAGTCGTAAACAAGTTCCGTAGTGAACCTCGCGAAGAGATCATATTGAAT	60
Oy	68	GAATATAGAGTTGGTTGTCGCTGCAGCTCCGCGAGAGCATGTCCACGCTTCTCTTCATC	127
Db	61	GAATATAGAGTTGGTTGTCGCTGCAGCTCCGCGAGAGCATGTCCACGCTTCTCTTCATC	120
Oy	128	CACACACACCTGTGACGTTGTGAGACGAGACCGCTAAAAAGTCTTCGCTATTAAAC	187
Db	121	CACACACACCTGTGACGTTGTGAGACGAGACCGCTAAAAAGTCTTCGCTATTAAAC	180
Oy	188	CACACAAACCCCATGTATTTTAAATTTGAATGTAATGTTATACCATCATTTAAAC	245
Db	181	CACACAAACCCCATGTATTTTAAATTTGAATGTAATGTTATACCATCATTTAGAACT	238

[illegible]

BASE COUNT	/note="Internal transcribed spacer 2, (ITS2)"				
ORIGIN	168 a	131 c	143 g	195 t	
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Best Local Similarity	98.7%; Pred. No. 5.2e-53;				
Matches 233;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;	
OY	5	AGGGGAATTA	AAAAAGTCGTAC	AGAGTTCCTCGTAGTGAACCTCGCGGANGAGATCATTTATTC	64
Db	1	AGAGGAGACT	TA	AAAAAGTCGTACAGAGTTCCTCGTAGTGAACCTCGCGGANGAGATCATTTATTC	60
OY	65	AATGAATAT	TAGAGTGTGGTTGCGTGCCTCCTCCGCGGAGCATGTCACAGCTTTCTCTTC	124	
Db	61	AATGAATAT	TAGAGTGTGGTTGCGTGCCTCCTCCGCGGAGCATGTCACAGCTTTCTCTTC	120	
OY	125	ATCCACACAC	ACTCTGTGCACCTGTGAGACGAGGAGACCGTAA	AAAAAGTCCTCCGCTATTTA	184
Db	121	ATCCACACAC	ACTCTGTGCACCTGTGAGACGAGGAGACCGTAA	AAAAAGTCCTCCGCTATTTA	180
OY	185	AACCAACA	AAACCCCATTTGATTTAAATTTGAATTTGAATTTGATTTAAACCATCATTA	240	
Db	181	AACCAACA	AAACCCCATTTGATTTAAATTTGAATTTGATTTGATTTAAACCATCATTA	236	

RESULT 7	
RSP242885	
LOCUS	RSP242885
DEFINITION	Rhizoctonia sp. Eab-S5 5.8S rRNA gene and ITS1 and 2, strain Eab-S5.
ACCESSION	RSP242885
VERSION	AJ242885.1 GI:18181607
KEYWORDS	5.8S ribosomal RNA; 5.8S rRNA gene; Internal transcribed spacer 1; internal transcribed spacer 2, ITS1, ITS2.
SOURCE	Rhizoctonia sp. Eab-S5.
ORGANISM	Rhizoctonia sp.
REFERENCE	Eukaryota, Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes; Heterobasidiomycetidae; Ceratobasidiales; Ceratobasidiaceae; mitosporic Ceratobasidiaceae; Rhizoctonia.
AUTHORS	1 Salazar, O., Munoz, R., Lopez-Corcoles, H. and Rubio, V.
TITLE	Molecular characterization and pathogenicity of a new group of isolates of binucleate Rhizoctonia spp. (Ceratobasidium spp.) isolated in Spain
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 660)
AUTHORS	Julian, M.C.
TITLE	Direct Submission
JOURNAL	Submitted (02-JUN-1999) Julian M.C., Departamento de Biotecnologia Microbiana, Centro Nacional de Biotecnologia, Campus Cantoblanco, Universidad Autonoma de Madrid, Madrid 28049, SPAIN
FEATURES	Location/Qualifiers
source	1..660
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	/strain="Eab-S5"
	/db_xref="taxon:183689"
	/country="Spain"
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gene	237..391
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rRNA	237..391
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misc_feature	392..>660
	/note="Internal transcribed spacer 2, (ITS2)"
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Query Match	93.8%; score 229.8; DB 8; Length 660;
Best Local Similarity	99.1%; Pred. No. 1,3e-52;
Matches 231; Conservative	0; Mismatches 2; Indels 0; Gaps 0;

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QY	73	TAGAAGTTGGTATTCGCTCGCTCTCCGGAGACATGTGCACGCTCTTCTTCATCCACAC	132
Db	64	TAGAAGTTGGTATTCGCTCGCTCTCCGGAGAGATGTGCACGCTTCTCTTTCATCCACAC	123
QY	133	ACACCTGTGCACCTTGTGACACGAGAGACCGTAAAAAAGTCTTCCGTCATTTAAACCAAC	192
Db	124	ACACCTGTGCACCTTGTGACGAGGAGACCGTAAAAAAGTCTTCCGTCATTTAAACCAAC	183
QY	193	AAACCCCTTTGATTTAAATTGAATGTATTTAGTGAACGATCATCTTTAAACCT	245
Db	184	AAACCCCAATGTATTTAAATTGAATGTATTTAGTGAACGATCATCTTTAAACCT	236

RESULT	8			
RSP242886				
LOCUS				
DEFINITION	RSP242886	661 bp	DNA	linear
	Rhizoctonia sp. Eab-S6	5.8S rRNA gene and ITS1 and 2, strain Eab-S6		PLN 15-JAN-200
ACCESSION	AJ242886			
VERSION	AJ242886.1	GI:18181608		
KEYWORDS	5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer 1; internal transcribed spacer 2; ITS1; ITS2.			
SOURCE	Rhizoctonia sp. Eab-S6			
ORGANISM	Rhizoctonia sp. Eab-S6			

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

1
Salazar, O., Munoz, R., Lopez-Corcoles, H. and Rubio, V.
Molecular characterization and pathogenicity of a new group of
isolates of binucleate *Rhizoctonia* spp. (*Ceratobasidium* spp.)
isolated in Spain
unpublished
2 (bases 1 to 661)
Julian, M.C.
Direct Submission
Submitted (02-JUN-1999) Julian M.C., Departamento de Biotecnologia

FEATURES	Location/Qualifiers
source	1. .661

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    /strain="Eab-S6"
    /db_xref="taxon:183690"
    /country="Spain"
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Db 6 AAAGTCGTACCAAGTTTCCGTAGGTGAACCTGCCGAAGGATCATTTATGAATGAATAT 65

QY 74 AGAGTTGGTTGTCGCTCGCTCCGGAGCATGTGCACGCTTCTCTTCATCCACACA 133

Db 66 AGAGTTGTTGTCGCTCCTCCGGAGCATGTGCACGCTTCTCTTCATCCACACA 125

OY 134 CACCTGTGCATTGAGAGCGGAGACCCTAAAAAGTCTCCGCTATTTAAACCAACA 193
 ||| |
Db 126 CACGTCGTGACTTGAGAGCGGAGACCCTAAAAAAGTCTCCGCTATTTAAACCAACA 185

QY 194 AACCCCATTTGTAATTAATGTAATGTAATGTAACGCATCAATTAACACT 245
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 186 AACCCCATCGTAATTAAGTTGAATGTAATGTAACGCATCAATTAAGAACT 237
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RESULT 9
RSP242881
2000120001
CCF 10
END
11:00:00
END 11
END 2000

LOCUS	RSP242881	665 bp	DNA	linear	PLN 15-JAN-2002
DEFINITION	Rhizoctonia sp. Eab-S1 5.8S rRNA gene and ITS1 and 2, strain Eab-S1.				
ACCESSION	AF242881				
VERSION	AF242881.1	GI:18181603			
KEYWORDS	5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer 1; internal transcribed spacer 2; ITS1; ITS2.				

ORGANISM
Rhizoctonia sp. Fab-S1
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Heterobasidiomycetidae; Ceratobasidiales;
Ceratobasidiaceae; mitosporic Ceratobasidiaceae; Rhizoctonia.
1

REFERENCE

TITLE	JOURNAL	REFERENCE
Molecular characterization and pathogenicity of a new group of isolates of binucleate Rhizoctonia spp. (Ceratobasidium spp.) isolated in Spain	Unpublished	2 (bases 1 to 665)

TITLE	Direct Submission
JOURNAL	Submitted (02-JUN-1999) Julian M.C., Departamento de Biotecnología, Microbiología, Centro Nacional de Biotecnología, Campus Cantoblanco, Universidad Autónoma de Madrid, Madrid 28049, SPAIN
FEATURES	Location/Qualifiers

FEATURES	
source	Location/Qualifiers
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77 GTTGGTTGTGGCTGCTC-CGGAGCATGTGCACGCTTTCTCTTCAATCCACACACA 135

22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051

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Db 181 CCCCATGTATTTAAATTGAATGTATTGATGTACCGCATCATTAGAACT 230

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DEFINITION Rhizoctonia sp. C-653 5.8S rRNA gene and ITS1 and 2, strain C-653.
ACCESSION AJ242897
VERSION AJ242897.1 GI:18181854
KEYWORDS 5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer 1; internal transcribed spacer 2; ITS1; ITS2.
SOURCE Rhizoctonia sp. C-653
ORGANISM Rhizoctonia sp. C-653
REFERENCE Salazar, O., Munoz, R., Lopez-Corcoles, H. and Rubio, V.
AUTHORS Molecular characterization and pathogenicity of a new group of
TITLE isolates of binucleate Rhizoctonia spp. (Ceratobasidium spp.)
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 659)
AUTHORS Julian, M.C.
-TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Julian M.C., Departamento de Biotecnologia
Microbiologia, Centro Nacional de Biotecnologia, Campus Cantoblanco,
Universidad Autonoma de Madrid, Madrid 28049, SPAIN
LOCATION/Qualifiers
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QY 65 AATGAATTAAGTGTGTTGCTGCTGCTC-CTCCGGAGAGATGTGACAGCTTTCTCTT 123
DB 73 AATGAATTAAGTGTGTTGCTGCTGCTGCTTTCACGGGGATGTGACAGCTTCTCTT 132
QY 124 CATCCACACACACCTGTCATCTGTGAGAGGAGGACGCTAAAGAGCTTCCGCTATT 183
DB 133 CATCCACACACACCTGTCATCTGTGAGAGGAGG- GCTTAATTAATTAAGTCTCGCTATT 191
QY 184 AAACACACAAACCCCATTTATTTAATTAATTAATTAATTAATTAATTAATTAATTA 243
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DB 251 CT 252

ACCESSION AJ242898
VERSION AJ242898.1 GI:18181855
KEYWORDS 5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer 1; internal transcribed spacer 2; ITS1; ITS2.
SOURCE Rhizoctonia sp. AV-2
ORGANISM Rhizoctonia sp. AV-2
REFERENCE Salazar, O., Munoz, R., Lopez-Corcoles, H. and Rubio, V.
AUTHORS Molecular characterization and pathogenicity of a new group of
TITLE isolates of binucleate Rhizoctonia spp. (Ceratobasidium spp.)
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 661)
AUTHORS Julian, M.C.
-TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Julian M.C., Departamento de Biotecnologia
Microbiologia, Centro Nacional de Biotecnologia, Campus Cantoblanco,
Universidad Autonoma de Madrid, Madrid 28049, SPAIN
LOCATION/Qualifiers
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DB 12 AGAGGAAGTAAAGTCGTACAGAGTTTCGTAGTGAACCTGCGGAGAGATCATTTATG 71
QY 65 AATGAATTAAGTGTGTTGCTGCTGCTC-CCGGAGAGATGTGACAGCTTCTCTT 122
DB 72 AATGAAGTAAAGTGTGTTGCTGCTGCTTTCACCTGAGGATGTGACAGCTTCTCTT 131
QY 123 TCATCCACACACCTGTCATCTGTGAGAGGAGAGAGCCGTTAAAGTCTTCTCTAT 182
DB 132 TCATCCACACACACCTGTCATCTGTGAGAGGAGG- GCTTAATTAATTAAGTCTTCTCTAC 190
QY 183 TAAACACACAAACCCCATTTATTTAATTAATTAATTAATTAATTAATTAATTAATTA 242
DB 191 TTAATCCACAAACTC--ATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 248
QY 243 ACT 245
DB 249 ACT 251

RESULT 12
RSP242899
LOCUS RSP242899 661 bp DNA linear PLN 15-JAN-2002
DEFINITION Rhizoctonia sp. 184 5.8S rRNA gene and ITS1 and 2, strain 184.
ACCESSION AJ242899
VERSION AJ242899.1 GI:18181856
KEYWORDS 5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer 1; internal transcribed spacer 2; ITS1; ITS2.
SOURCE Rhizoctonia sp. 184.

ORGANISM Rhizoctonia sp. 184
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Heterobasidiomycetidae; Ceratobasidiales;
Ceratobasidiaceae; mitosporic Ceratobasidiaceae; Rhizoctonia.

REFERENCE 1
AUTHORS Salazar O., Munoz R., Lopez-Corcoles H. and Rubio V.
TITLE Molecular characterization and pathogenicity of a new group of isolates of binucleate Rhizoctonia spp. (Ceratobasidium spp.) isolated in Spain
JOURNAL unpublished
AUTHORS 2 (bases 1 to 661)
JOURNAL Julian M.C.
REFERENCE Direct Submission
TITLE Submitted (02-JUN-1999) Julian M.C., Departamento de Biología Microbiana, Centro Nacional de Biotecnología, Campus Cantolablanco, Universidad Autónoma de Madrid, Madrid 28049, SPAIN
JOURNAL location/Qualifiers

FEATURES
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rRNA 252..406
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BASE COUNT 184 a 134 c 140 g 203 t
ORIGIN

Query Match 67.8%; Score 166.2; DB 8; Length 661;
Best Local Similarity 88.5%; Pred. No. 3.5e-35;
Matches 215; Conservative 0; Mismatches 23; Indels 5; Gaps 3;

QY 5 AGGGGAATAAAGTCTGAACAAGTTCCGTAGTGAACCTGCGAAGATCATTTATG 64
Db 12 AGAGGAATAAAGTCTGAACAAGTTCCGTAGTGAACCTGCGAAGATCATTTATG 71
QY 65 AATGAATATAGTGGTGTGCTGCTGCT--CCGGAGCATGTGCAGCTTCTCTT 122
Db 72 AATGAATATAGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTT 131
QY 123 TCATCCACACACCTGTGCACTGTGAGAGCGAGACCGTAAAGTCTTCGCTCAT 182
Db 132 TCATCCACACACCTGTGCACTGTGAGAGCGAGG--GCTTTAATTAATGCTTCGCTCAT 190
QY 183 TAAACACACAAACCCCATTTGATTAATTAATTAATTAATTAATTAATTAATTA 242
Db 191 TTAATCAACAACCTC--ATTATTAATTAATTAATTAATTAATTAATTAATTAATTA 248
QY 243 ACT 245
Db 249 ACT 251

RESULT 13
RSP242892 661 bp DNA linear PLN 15-JAN-2002
LOCUS Rhizoctonia sp. SIR-2 5.8S rRNA gene and ITS1 and 2, strain SIR-2.
DEFINITION Rhizoctonia sp. SIR-2 5.8S rRNA gene and ITS1 and 2, strain SIR-2.
ACCESSION AJ242892
VERSION AJ242892.1 GI:18181849
KEYWORDS 5.8S ribosomal RNA; 5.8S rRNA gene; Internal transcribed spacer 1; Internal transcribed spacer 2; ITS1; ITS2.
SOURCE Rhizoctonia sp. SIR-2.
ORGANISM Rhizoctonia sp. SIR-2.
REFERENCE Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Heterobasidiomycetidae; Ceratobasidiales;
Ceratobasidiaceae; mitosporic Ceratobasidiaceae; Rhizoctonia.

AUTHORS Salazar O., Munoz R., Lopez-Corcoles H. and Rubio V.
TITLE Molecular characterization and pathogenicity of a new group of isolates of binucleate Rhizoctonia spp. (Ceratobasidium spp.) isolated in Spain
JOURNAL unpublished
AUTHORS 2 (bases 1 to 661)
JOURNAL Julian M.C.
REFERENCE Direct Submission
TITLE Submitted (02-JUN-1999) Julian M.C., Departamento de Biología Microbiana, Centro Nacional de Biotecnología, Campus Cantolablanco, Universidad Autónoma de Madrid, Madrid 28049, SPAIN
JOURNAL location/Qualifiers

FEATURES
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gene 257..411
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rRNA 257..411
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misc_feature 412..>661
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BASE COUNT 180 a 140 c 142 g 199 t
ORIGIN

Query Match 58.8%; Score 144; DB 8; Length 661;
Best Local Similarity 80.4%; Pred. No. 4.3e-29;
Matches 193; Conservative 0; Mismatches 45; Indels 2; Gaps 2;

QY 5 AGGGGAATAAAGTCTGAACAAGTTCCGTAGTGAACCTGCGAAGATCATTTATG 64
Db 15 AGAGGAATAAAGTCTGAACAAGTTCCGTAGTGAACCTGCGAAGATCATTTATG 74
QY 65 AATGAATATAGTGGTGTGCTGCTGCT--CCTCGGAGCATGTGCAGCTTCTCT-T 122
Db 75 AATGAATATAGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTT 134
QY 123 TCATCCACACACCTGTGCACTGTGAGAGCGAGACCGTAAAGTCTTCGCTCAT 182
Db 135 TCATCCACACACCTGTGCACTGTGAGAGCGAGACCGTAAAGTCTTCGCTCAT 194
QY 183 TAAACACACAAACCCCATTTGATTAATTAATTAATTAATTAATTAATTAATTA 242
Db 195 AATTCATATACAAACCTCATTTAATTAATTAATTAATTAATTAATTAATTAATTA 254

RESULT 14
RSP242902 694 bp DNA linear PLN 15-JAN-2002
LOCUS Rhizoctonia sp. TCI 5.8S rRNA gene and ITS1 and 2, strain TCI.
DEFINITION Rhizoctonia sp. TCI 5.8S rRNA gene and ITS1 and 2, strain TCI.
ACCESSION AJ242902
VERSION AJ242902.1 GI:18181859
KEYWORDS 5.8S ribosomal RNA; 5.8S rRNA gene; Internal transcribed spacer 1; Internal transcribed spacer 2; ITS1; ITS2.
SOURCE Rhizoctonia sp. TCI.
ORGANISM Rhizoctonia sp. TCI.
REFERENCE Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Heterobasidiomycetidae; Ceratobasidiales;
Ceratobasidiaceae; mitosporic Ceratobasidiaceae; Rhizoctonia.

REFERENCE 1
AUTHORS Salazar O., Munoz R., Lopez-Corcoles H. and Rubio V.
TITLE Molecular characterization and pathogenicity of a new group of isolates of binucleate Rhizoctonia spp. (Ceratobasidium spp.) isolated in Spain
JOURNAL unpublished
AUTHORS 2 (bases 1 to 694)
JOURNAL Julian M.C.
REFERENCE Direct Submission
TITLE Submitted (02-JUN-1999) Julian M.C., Departamento de Biotecnología

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: March 2, 2003, 05:44:08 ; Search time 129 Seconds
(without alignments)
4277.051 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	238.6	97.4	401	21	AAZ92451 Rhizoctonia sp. is
3	235.4	96.1	407	21	AAZ92452 Rhizoctonia sp. is
4	234.6	95.8	398	21	AAZ92446 Rhizoctonia sp. is
5	231.6	94.5	393	21	AAZ92447 Rhizoctonia sp. is
6	231.4	94.4	405	21	AAZ92445 Rhizoctonia sp. is
7	229.8	93.8	391	21	AAZ92448 Rhizoctonia sp. is
8	225.6	92.1	392	21	AAZ92449 Rhizoctonia sp. is
9	216.4	88.3	385	21	AAZ92453 Rhizoctonia sp. is

10	173	70.6	408	21	AAZ92468 Rhizoctonia sp. is
11	166.2	67.8	406	21	AAZ92467 Rhizoctonia sp. is
12	144	58.8	411	21	AAZ92465 Rhizoctonia sp. is
13	142.6	58.2	409	21	AAZ92463 Rhizoctonia sp. is
14	140.8	57.5	411	21	AAZ92466 Rhizoctonia sp. is
15	133.6	54.5	410	21	AAZ92464 Rhizoctonia sp. is
16	128	52.2	385	21	AAZ92460 Rhizoctonia sp. is
17	122	49.8	381	21	AAZ92455 Rhizoctonia sp. is
18	117.2	47.8	412	21	AAZ92469 Rhizoctonia sp. is
19	116.2	47.4	394	21	AAZ92458 Rhizoctonia sp. is
20	114.8	46.9	387	21	AAZ92454 Rhizoctonia sp. is
21	112	45.7	415	21	AAZ92472 Rhizoctonia sp. is
22	106.2	43.3	415	21	AAZ92473 Rhizoctonia sp. is
23	105	42.9	413	21	AAZ92470 Rhizoctonia sp. is
24	104.8	42.8	416	21	AAZ92462 Rhizoctonia sp. is
25	103.4	42.2	413	21	AAZ92471 Rhizoctonia sp. is
26	98.2	40.1	414	21	AAZ92475 Rhizoctonia sp. is
27	92.4	37.7	416	21	AAZ92474 Rhizoctonia sp. is
28	84.6	34.5	328	21	AAZ92459 Rhizoctonia sp. is
29	83.8	34.2	684	22	AAZ92458 Rhizoctonia sp. is
30	80.6	32.9	685	22	AAZ92457 Rhizoctonia sp. is
31	72.8	29.7	686	22	AAZ92456 Rhizoctonia sp. is
32	69.6	28.4	686	22	AAZ92455 Rhizoctonia sp. is
33	69.6	28.4	686	22	AAZ92454 Rhizoctonia sp. is
34	69.6	28.4	686	22	AAZ92453 Rhizoctonia sp. is
35	69.6	28.4	687	22	AAZ92452 Rhizoctonia sp. is
36	69.6	28.4	687	22	AAZ92451 Rhizoctonia sp. is
37	69.6	28.4	687	22	AAZ92450 Rhizoctonia sp. is
38	69.6	28.4	687	22	AAZ92449 Rhizoctonia sp. is
39	69.6	28.4	687	22	AAZ92448 Rhizoctonia sp. is
40	68.4	27.9	428	21	AAZ92457 Rhizoctonia sp. is
41	67.4	27.5	429	21	AAZ92456 Rhizoctonia sp. is
42	62.4	25.5	675	22	AAZ92482 Rhizoctonia sp. is
43	60.8	24.3	357	21	AAZ92482 Rhizoctonia sp. is
44	57	23.3	253	22	AAZ92482 Rhizoctonia sp. is
45	55.2	22.5	3420	24	ABA99033 Saccharomyces cere

ALIGNMENTS

RESULT 1	AAZ92450	AAZ92450 standard; DNA; 400 BP.
ID	AAZ92450	
XX	AAZ92450:	
AC	AAZ92450:	
XX	05-JUN-2000 (first entry)	
DT	05-JUN-2000 (first entry)	
XX	Rhizoctonia sp. isolate Eab-F1 ribosomal DNA, ITS1-5.8s region.	
DE	Rhizoctonia sp. isolate Eab-F1 ribosomal DNA, ITS1-5.8s region.	
XX	Antifungal; biocontrol; binucleate; non-pathogenic fungus;	
KW	Strain identification; classification; internal transcribed spacer;	
KW	ITS region; 5.8s region; ribosomal; ds.	
XX	Rhizoctonia sp.	
OS	Rhizoctonia sp.	
XX	WO200004779-A1.	
PN	WO200004779-A1.	
XX	03-FEB-2000.	
PD	03-FEB-2000.	
XX	23-JUL-1999; 99WO-GB02406.	
PF	23-JUL-1999; 99WO-GB02406.	
XX	24-JUL-1998; 98GB-0016265.	
PR	24-JUL-1998; 98GB-0016265.	
XX	(TECN-) INST TECNICO AGRONOMICO PROVINCIAL SA.	
PA	(RUEF/) RUEFLES G K.	
PA	(RUEF/) RUEFLES G K.	
XX	Rubio Susan V, Salazar Torres O, Julian Esquivias M;	
PI	Gonzales Garcia V, Gomez-Acebo Gullon E, Munoz Gomez R;	
PI	Lopez Corcoles H;	
PI	Lopez Corcoles H;	
XX	WPI; 2000-182492/16.	

XX Protection of plants including tomato, pepper, lettuce, radish,
PT parsley, sugar beet, rape, and onions against pathogenic fungi, uses a
PT binucleate Rhizoctonia strain for biocontrol
PS Claim 5; Fig 1; 121pp; English.
XX
CC The invention relates to a novel method of protecting plants from
CC pathogenic fungi. The method comprises biocontrol of pathogenic fungi
CC via the use of a non-pathogenic, binucleate Rhizoctonia strain. The
CC binucleate Rhizoctonia is selected by molecular detection of certain
CC internal transcribed spacer (ITS)-5.8s ribosomal DNA sequences
CC (AA292445-AA292458), which vary between strains of these fungi. The
CC invention also encompasses a concentrate for use in plant protection
CC containing viable material from the binucleate Rhizoctonia strains of the
CC invention, and primers (AA292437-292444) for identifying these strains.
CC The strains of the invention are used as biocontrol agents for related
CC pathogenic fungi. Binucleate Rhizoctonia isolate Eab-F2 was tested for
CC its ability to protect tomato seedlings from the pathogenic Rhizoctonia
CC strain Web.2. The Rhizoctonia strains were inoculated either
CC simultaneously or consecutively (the binucleate strain followed by the
CC pathogenic strain), and the protection effect indicated by the degree of
CC infected vegetal surface. The binucleate strain was found to provide
CC protection against the pathogenic strain when it had been allowed to
CC colonise the vegetal surface prior to pathogenic fungal infection (i.e.,
CC consecutive inoculation), whereas no protection was provided when both
CC strains were inoculated simultaneously. The method of the invention may
CC be used to protect a wide variety of plants from pathogenic fungal
CC infection. Plants that may be protected include vegetables, crops such as
CC oilseed rape, sugar beet and alfalfa, trees and ornamental plants. The
CC method is reliable and provides economical biocontrol of diseases caused
CC by Rhizoctonia solani. Sequences AA292445-292458 represent the ITS-5.8s
CC regions of ribosomal RNA-encoding DNA from the novel non-pathogenic
CC binucleate Rhizoctonia strains of the invention.
XX
SQ Sequence 400 BP; 116 A; 83 C; 88 G; 113 T; 0 other;
Query Match 100.0%; Score 245; DB 21; Length 400;
Best Local Similarity 100.0%; Pred. No. 3.8e-71;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTAGAGGGGAATTAATAAGCTGTACACAGCTTCCGTAGGTGAACCTGGGAGATCATTT 60
DB 1 TTAGAGGGGAATTAATAAGCTGTACACAGCTTCCGTAGGTGAACCTGGGAGATCATTT 60
QY 61 ATTGAATGAATATATAGATTGCTGCTGCTCTCCGGGAGCATGTGCACGCTTTCTC 120
DB 61 ATTGAATGAATATATAGATTGCTGCTGCTCTCCGGGAGCATGTGCACGCTTTCTC 120
QY 121 TTTTCATCCACACACCTGTGACACTTGTGAGACGAGACCGTAATAAAGTCTCCGCT 180
DB 121 TTTTCATCCACACACCTGTGACACTTGTGAGACGAGACCGTAATAAAGTCTCCGCT 180
QY 181 ATTAACCAACCAACCCCATTTGTAATTAATTTGAATGTAATGTAACGCATCATTA 240
DB 181 ATTAACCAACCAACCCCATTTGTAATTAATTTGAATGTAATGTAACGCATCATTA 240
QY 241 AAACCT 245
DB 241 AAACCT 245

KW strain identification; classification; internal transcribed spacer;
KW ITS region: 5.8s region; ribosomal; ds.
XX Rhizoctonia sp.
OS
XX WO200004779-A1.
XX
XX 03-FEB-2000.
XX
XX 23-JUL-1999; 99WO-GB02406.
XX
XX 24-JUL-1998; 98GB-0016265.
XX
XX (TECN-) INST TECNICO AGRONOMICO PROVINCIAL SA.
XX (RUFFE) RUFFLES G K.
XX Rubio Susan V, Salazar Torres O, Julian Esquivias M,
PI Gonzales Garcia V, Gomez-Acebo Gullon E, Munoz Gomez R;
PI Lopez Corcoles H;
XX WPI: 2000-182492/16.
XX
XX Protection of plants including tomato, pepper, lettuce, radish,
PT parsley, sugar beet, rape, and onions against pathogenic fungi, uses a
PT binucleate Rhizoctonia strain for biocontrol
PS Claim 5; Fig 1; 121pp; English.
XX
CC The invention relates to a novel method of protecting plants from
CC pathogenic fungi. The method comprises biocontrol of pathogenic fungi
CC via the use of a non-pathogenic, binucleate Rhizoctonia strain. The
CC binucleate Rhizoctonia is selected by molecular detection of certain
CC internal transcribed spacer (ITS)-5.8s ribosomal DNA sequences
CC (AA292445-AA292458), which vary between strains of these fungi. The
CC invention also encompasses a concentrate for use in plant protection
CC containing viable material from the binucleate Rhizoctonia strains of the
CC invention, and primers (AA292437-292444) for identifying these strains.
CC The strains of the invention are used as biocontrol agents for related
CC pathogenic fungi. Binucleate Rhizoctonia isolate Eab-F2 was tested for
CC its ability to protect tomato seedlings from the pathogenic Rhizoctonia
CC strain Web.2. The Rhizoctonia strains were inoculated either
CC simultaneously or consecutively (the binucleate strain followed by the
CC pathogenic strain), and the protection effect indicated by the degree of
CC infected vegetal surface. The binucleate strain was found to provide
CC protection against the pathogenic strain when it had been allowed to
CC colonise the vegetal surface prior to pathogenic fungal infection (i.e.,
CC consecutive inoculation), whereas no protection was provided when both
CC strains were inoculated simultaneously. The method of the invention may
CC be used to protect a wide variety of plants from pathogenic fungal
CC infection. Plants that may be protected include vegetables, crops such as
CC oilseed rape, sugar beet and alfalfa, trees and ornamental plants. The
CC method is reliable and provides economical biocontrol of diseases caused
CC by Rhizoctonia solani. Sequences AA292445-292458 represent the ITS-5.8s
CC regions of ribosomal RNA-encoding DNA from the novel non-pathogenic
CC binucleate Rhizoctonia strains of the invention.
XX
SQ Sequence 401 BP; 116 A; 83 C; 88 G; 114 T; 0 other;
Query Match 97.4%; Score 238.6; DB 21; Length 401;
Best Local Similarity 98.4%; Pred. No. 5e-69;
Matches 241; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 TTAGAGGGGAATTAATAAGCTGTACACAGCTTCCGTAGGTGAACCTGGGAGATCATTT 60
DB 2 TTAGAGGGGAATTAATAAGCTGTACACAGCTTCCGTAGGTGAACCTGGGAGATCATTT 61
QY 61 ATTGAATGAATATATAGATTGCTGCTGCTCTCCGGGAGCATGTGCACGCTTTCTC 120
DB 62 ATTGAATGAATATATAGATTGCTGCTGCTCTCCGGGAGCATGTGCACGCTTTCTC 121
QY 121 TTTTCATCCACACACCTGTGACACTTGTGAGACGAGACCGTAATAAAGTCTCCGCT 180
DB 122 TTTTCATCCACACACCTGTGACACTTGTGAGACGAGACCGTAATAAAGTCTCCGCT 181

	AC	AA692445; (first entry)
	AD	
	AE	Rhizoctonia sp. isolate Eab-F2 ribosomal DNA, ITS-1.8S region.
	AF	
	AG	Antifungal biocontrol; binucleate non-pathogenic fungus;
	AH	strain identification; classification; internal transcribed spacer:
	AI	ITS region; 5.8S region; ribosomal; ds.
	AJ	
	AK	Rhizoctonia sp.
	AL	
	AM	M0200004779-AI.
	AN	
	AO	03-FEB-2000.
	AP	
	AQ	23-JUL-1999; 99MO-BR02406.
	AR	
	AS	24-JUL-1998; 98GB-0016265.
	AT	(TECN-) INST TECNICO AGRONOMO PROVINCIAL SA.
	AV	(ROFF) ROFFLES G K.
	AW	Rubio Susan V, Salazar Torres O, Julian Esquivias M;
	AX	Gonzalez Garcia V, Gomez-Acebo Gullon E, Munoz Gomez R;
	AY	Lopez Corcoles H;
	BZ	WPJ; 2000-182492/16.
	CX	
	DY	Protection of plants including tomato, pepper, lettuce, radish,
	EZ	parsley, sugar beet, rape, and onions against pathogenic fungi, uses a
	FZ	binucleate Rhizoctonia strain for biocontrol -
	GZ	
	HZ	Claim 5; Fig 1; 12pp; English.
	IZ	
	JZ	The invention relates to a novel method of protecting plants from
	KZ	pathogenic fungi. The method comprises biocontrol of pathogenic fungi
	LZ	via the use of a non-pathogenic, binucleate Rhizoctonia strain. The
	MZ	CC binucleate Rhizoctonia is selected by molecular detection of certain
	NZ	internal transcribed spacer (ITS)-5.8S ribosomal DNA sequences
	OZ	(AA292445- AA292458), which vary between strains of these fungi. The
	PZ	invention also encompasses a concentrate for use in plant protection
	QZ	containing viable material from the binucleate Rhizoctonia strains of the
	RZ	invention, and primers (AA292437-292444) for identifying these strains.
	SZ	CC The strains of the invention are used as biocontrol agents for related
	TZ	pathogenic fungi. Binucleate Rhizoctonia isolate Eab-F2 was tested for
	VZ	its ability to protect tomato seedlings from the pathogenic Rhizoctonia
	XZ	strain Me8.2. The Rhizoctonia strains were inoculated either
	YZ	simultaneously or consecutively (the binucleate stain followed by the
	ZZ	pathogenic strain), and the protection effect indicated by the degree of
		infected vegetal surface. The binucleate strain was found to provide
		protection against the pathogenic strain when it had been allowed to
		colonise the vegetal surface prior to pathogenic fungal infection (i.e.,
		consecutive inoculation), whereas no protection was provided when both
		strains were inoculated simultaneously. The method of the invention may
		be used to protect a wide variety of plants from pathogenic fungi
		infection. Plants that may be protected include vegetables, crops such as
		oilseed rape, sugar beet and alfalfa, trees and ornamental plants. The
		method is reliable and provides economical biocontrol of diseases caused
		by Rhizoctonia solani. Sequences AA292445-292458 represent the ITS-5.8S
		regions of ribosomal RNA-encoding DNA from the novel non-pathogenic
		binucleate Rhizoctonia strains of the invention.
		Sequence 405 BP; 114 A; 83 C; 89 G; 111 T; 8 other;
		Query Match 94.4%; Score 231.4; DB 21; Length 405;
		Best Local Similarity 97.1%; Pred. No. 1.2e-66;
		Matches 233; Conservative 1; Mismatches 6; Indels 0; Gaps 0
		1 TTGAGGGGAATTAAAGCTGTACAAGTTTCCTAGTGACTCGGAGAAGTCAATT 60
		II III III III III III III III III III III III III III III III
		5 DNNNAGGAGCAATAAAGTCGTACCAAGTTTCCTAGTAAACCCTGGGAGCATTAAT 64

OY	61	ATTGAATGAATATAGAGTTGGTGTGGCGTGGCTCCCGGAGACATGTGACGGCTTTCTC	120
Db	65	ATTGAATGAATATAGAGTTGGTGTGGCGTGGCTCCCGGAGACATGTGACGGCTTTCTC	124
OY	121	TTTCATCCACACACACCTGTGCTGCTGTGATGACGGAGACCGTAAATAAGCTTCCGCT	180
Db	125	TTTCATCCACACACACCTGTGCTGCTGTGATGACGGAGACCGTAAATAAGCTTCCGCT	184
OY	181	ATTAAACCCACACAAACCCATTGTATTTAAATTTGAATGTATGTATGATTAACGATCATTA	240
Db	185	ATTAAACCCACACAAACCCATTGTATTTAAATTTGAATGTATGTATGATTAACGATCATTA	244
RESULT 7			
AAZ92448			
ID	AAZ92448	standard; DNA; 391 BP.	
XX			
AC	AAZ92448;		
XX			
DT	05-JUN-2000	(first entry)	
XX			
DE	Rhizoctonia sp. isolate Eab-S5 ribosomal DNA, ITS1-5.8s region.		
XX			
KW	Antifungal: biocontrol; binucleate; non-pathogenic fungi;		
KW	strain identification; classification; internal transcribed spacer;		
KW	ITS region; 5.8s region; ribosomal; ds.		
XX			
OS	Rhizoctonia sp.		
PN	MO200004779-A1.		
XX			
PD	03-FEB-2000.		
XX			
PF	23-JUL-1999; 99WO-GB02406.		
PR	24-JUL-1998; 98GB-0016265.		
XX			
XX			
PA	(TECN-) INST TECNICO AGRONOMICO PROVINCIAL SA.		
PA	(RUFE/) RUFELES G K.		
PI	Rubio Susan V, Salazar Torres O, Julian Esquivias M;		
PI	Gonzalez Garcia V, Gomez-Acebo Gullon E, Munoz Gomez R;		
PI	Lopez Corcoles H;		
DR	WPI: 2000-182492/16.		
XX			
PT	Protection of plants including tomato, pepper, lettuce, radish,		
PT	parsley, sugar beet, rape, and onions against pathogenic fungi, uses a		
PT	binucleate Rhizoctonia strain for biocontrol -		
XX			
PS	Claim 5; Fig 1; 121pp; English.		
CC	The invention relates to a novel method of protecting plants from		
CC	pathogenic fungi. The method comprises biocontrol of pathogenic fungi		
CC	via the use of a non-pathogenic, binucleate Rhizoctonia strain. The		
CC	binucleate Rhizoctonia is selected by molecular detection of certain		
CC	internal transcribed spacer (ITS)-5.8s ribosomal DNA sequences		
CC	AAZ92445- AAZ92458), which vary between strains of these fungi. The		
CC	invention also encompasses a concentrate for use in plant protection		
CC	containing viable material from the binucleate Rhizoctonia strains of the		
CC	invention, and primers (AAZ92437-292444) for identifying these strains.		
CC	The strains of the invention are used as biocontrol agents for related		
CC	pathogenic fungi. Binucleate Rhizoctonia isolate Eab-F2 was tested for		
CC	its ability to protect tomato seedlings from the pathogenic Rhizoctonia		
CC	strain Me8.2. The Rhizoctonia strains were inoculated either		
CC	simultaneously or consecutively (the binucleate strain followed by the		
CC	pathogenic strain), and the protection effect indicated by the degree of		
CC	infected vegetal surface. The binucleate strain was found to provide		
CC	protection against the pathogenic strain when it had been allowed to		
CC	colonize the vegetal surface prior to pathogenic fungal infection (i.e.,		
CC	consecutive inoculation), whereas no protection was provided when both		
CC	strains were inoculated simultaneously. The method of the invention may		
CC	be used to protect a wide variety of plants from pathogenic fungal		

CC Infection. Plants that may be protected include vegetables, crops such as
CC oilseed rape, sugar beet and alfalfa, trees and ornamental plants. The
CC method is reliable and provides economical biocontrol of diseases caused
CC by Rhizoctonia solani. Sequences AA292445-292458 represent the ITS-5.8s
CC regions of ribosomal RNA-encoding DNA from the novel non-pathogenic
CC binucleate Rhizoctonia strains of the invention.

XX Sequence 391 BP; 110 A; 83 C; 86 G; 112 T; 0 other;

SO Query Match 93.8%; Score 229.8; DB 21; Length 391;
Best Local Similarity 99.1%; Pred. No. 4.1e-66;
Matches 231; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 AAAAGTCGTAAACAGGTTTCCGTAGTGAACCTCGGAGAGATCATTTGAATGAATA 72

Db 4 ATTAAGTCGTAAACAGGTTTCCGTAGTGAACCTCGGAGAGATCATTTGAATGAATA 63

QY 73 TAGAGTTGGTGTGGCTGCTCCCGGAGACATGTGACGCTTCTCTTCATCCACAC 132

Db 64 TAGAGTTGGTGTGGCTGCTCCCGGAGACATGTGACGCTTCTCTTCATCCACAC 123

QY 133 ACACCTGTGCATCTGTGAGAGGAGACCGTAAAAAGTCTTCGTATTAAACACACAC 192

Db 124 ACACCTGTGCATCTGTGAGAGGAGACCGTAAAAAGTCTTCGTATTAAACACACAC 183

QY 193 AAACCCCATTTGATTTAATTGAATGTAATTGATGTAACGATCATTTAAACT 245

Db 184 AAACCCCATTTGATTTAATTGAATGTAATTGATGTAACGATCATTTGAACT 236

RESULT 8

AA292449 ID AA292449 standard; DNA; 392 BP.

XX AA292449;

XX 05-JUN-2000 (first entry)

XX Rhizoctonia sp. isolate Eab-s6 ribosomal DNA, ITS1-5.8s region.

XX Antifungal; biocontrol; binucleate; non-pathogenic fungus;

KW strain identification; classification; internal transcribed spacer;

KW ITS region; 5.8s region; ribosomal; ds.

XX Rhizoctonia sp.

XX OS WO200004779-A1.

XX 03-FEB-2000.

XX 23-JUL-1999; 99WO-GB02406.

XX 24-JUL-1998; 98GB-0016265.

XX (TECN-) INST TECNICO AGRONOMICO PROVINCIAL SA.

XX (RUFF/) RUFFLES G K.

XX Rubio Susan V, Salazar Torres O, Julian Esquivias M;

XX Gonzalez Garcia V, Gomez-Acebo Gullon E, Munoz Gomez R;

XX Lopez Corcoles H;

XX WPI; 2000-182492/16.

XX Protection of plants including tomato, pepper, lettuce, radish,

XX parsley, sugar beet, rape, and onions against pathogenic fungi, uses a

XX binucleate Rhizoctonia strain for biocontrol -

XX Claim 5; Fig 1; 121pp; English.

XX The invention relates to a novel method of protecting plants from

XX pathogenic fungi. The method comprises biocontrol of pathogenic fungi

XX via the use of a non-pathogenic, binucleate Rhizoctonia strain. The

XX binucleate Rhizoctonia is selected by molecular detection of certain

CC internal transcribed spacer (ITS)-5.8s ribosomal DNA sequences
CC (AA292445-AA292458), which vary between strains of these fungi. The
CC invention also encompasses a concentrate for use in plant protection
CC containing viable material from the binucleate Rhizoctonia strains of the
CC invention, and primers (AA292437-292444) for identifying these strains.

CC The strains of the invention are used as biocontrol agents for related

CC pathogenic fungi. Binucleate Rhizoctonia isolate Eab-F2 was tested for

CC its ability to protect tomato seedlings from the pathogenic Rhizoctonia

CC strain Me8.2. The Rhizoctonia strains were inoculated either

CC simultaneously or consecutively (the binucleate strain followed by the

CC pathogenic strain), and the protection effect indicated by the degree of

CC infected vegetal surface. The binucleate strain was found to provide

CC protection against the pathogenic strain when it had been allowed to

CC colonise the vegetal surface prior to pathogenic fungal infection (i.e.,

CC consecutive inoculation), whereas no protection was provided when both

CC strains were inoculated simultaneously. The method of the invention may

CC be used to protect a wide variety of plants from pathogenic fungal

CC infection. Plants that may be protected include vegetables, crops such as

CC oilseed rape, sugar beet and alfalfa, trees and ornamental plants. The

CC method is reliable and provides economical biocontrol of diseases caused

CC by Rhizoctonia solani. Sequences AA292445-292458 represent the ITS-5.8s

CC regions of ribosomal RNA-encoding DNA from the novel non-pathogenic

CC binucleate Rhizoctonia strains of the invention.

XX Sequence 392 BP; 110 A; 83 C; 89 G; 110 T; 0 other;

SO Query Match 92.1%; Score 225.6; DB 21; Length 392;
Best Local Similarity 98.3%; Pred. No. 1e-64;
Matches 228; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 14 AAAAGTCGTAAACAGGTTTCCGTAGTGAACCTCGGAGAGATCATTTGAATGAATA 73

Db 6 AAAAGTCGTAAACAGGTTTCCGTAGTGAACCTCGGAGAGATCATTTGAATGAATA 65

QY 74 AGAGTTGGTGTGGCTGCTCCCGGAGACATGTGACGCTTCTCTTCATCCACACA 133

Db 66 AGAGTTGGTGTGGCTGCTCCCGGAGACATGTGACGCTTCTCTTCATCCACACA 125

QY 134 CACCTGTGCATCTGTGAGAGGAGACCGTAAAAAGTCTTCGTATTAAACACACA 193

Db 126 CACCTGTGCATCTGTGAGAGGAGACCGTAAAAAGTCTTCGTATTAAACACACA 185

QY 194 AAACCCCATTTGATTTAATTGAATGTAATTGATGTAACGATCATTTAAACT 245

Db 186 AAACCCCATTTGATTTAATTGAATGTAATTGATGTAACGATCATTTAAACT 237

RESULT 9

AA292453 ID AA292453 standard; DNA; 385 BP.

XX AA292453;

XX 05-JUN-2000 (first entry)

XX Rhizoctonia sp. isolate Eab-s1 ribosomal DNA, ITS1-5.8s region.

XX Antifungal; biocontrol; binucleate; non-pathogenic fungus;

KW strain identification; classification; internal transcribed spacer;

KW ITS region; 5.8s region; ribosomal; ds.

XX Rhizoctonia sp.

XX OS WO200004779-A1.

XX 03-FEB-2000.

XX 23-JUL-1999; 99WO-GB02406.

XX 24-JUL-1998; 98GB-0016265.

XX (TECN-) INST TECNICO AGRONOMICO PROVINCIAL SA.

XX (RUFF/) RUFFLES G K.

XX XX Rubio Susan V, Salazar Torres O, Julian Esquivias M;
PI Gonzales Garcia V, Gomez-Acebo Gullon E, Munoz Gomez R;
PI Lopez Corcoles H;
XX WPI: 2000-182492/16.
DR
XX
XX Protection of plants including tomato, pepper, lettuce, radish,
PT parsley, sugar beet, rape, and onions against pathogenic fungi, uses a
PT binucleate *Rhizoctonia* strain for biocontrol.
XX
XX Claim 5, Fig 1; 121pp; English.
XX
XX The invention relates to a novel method of protecting plants from
CC pathogenic fungi. The method comprises biocontrol of pathogenic fungi
CC via the use of a non-pathogenic, binucleate *Rhizoctonia* strain. The
CC binucleate *Rhizoctonia* is selected by molecular detection of certain
CC internal transcribed spacer (ITS)-5.8s ribosomal DNA sequences
CC (AA92445- AA92458), which vary between strains of these fungi. The
CC invention also encompasses a concentrate for use in plant protection
CC containing viable material from the binucleate *Rhizoctonia* strains of the
CC invention, and primers (AA92437-292444) for identifying these strains.
CC The strains of the invention are used as biocontrol agents for related
CC pathogenic fungi. Binucleate *Rhizoctonia* isolate Eab-F2 was tested for
CC its ability to protect tomato seedlings from the pathogenic *Rhizoctonia*
CC strain Me8.2. The *Rhizoctonia* strains were inoculated either
CC simultaneously or consecutively (the binucleate strain followed by the
CC pathogenic strain), and the protection effect indicated by the degree of
CC infected vegetal surface. The binucleate strain was found to provide
CC protection against the pathogenic strain when it had been allowed to
CC colonise the vegetal surface prior to pathogenic fungal infection (i.e.,
CC consecutive inoculation), whereas no protection was provided when both
CC strains were inoculated simultaneously. The method of the invention may
CC be used to protect a wide variety of plants from pathogenic fungal
CC infection. Plants that may be protected include vegetables, crops such as
CC oilseed rape, sugar beet and alfalfa, trees and ornamental plants. The
CC method is reliable and provides economical biocontrol of diseases caused
CC by *Rhizoctonia solani*. Sequences AA92445-292458 represent the ITS-5.8s
CC regions of ribosomal RNA-encoding DNA from the novel non-pathogenic
CC binucleate *Rhizoctonia* strains of the invention.
XX
SQ Sequence 385 BP; 107 A; 83 C; 85 G; 110 T; 0 other;
Query Match 88.3%; Score 216.4; DB 21; Length 385;
Best Local Similarity 99.1%; Pred. No. 1.1e-61;
Matches 228; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 17 AGTGTACAGAGTTCGTAAGTAACTCGGAGAGATCATTTTAATGAATATGA 76
DB 1 AGTGTACAGAGTTCGTAAGTAACTCGGAGAGATCATTTTAATGAATATGA 60
QY 77 GTTGGTTGCGTGGCTCCTC-CGGAGACATGTGCAGCTTTCTTCATCCACACACA 135
DB 61 GTTGGTTGCGTGGCTCCTCCTCGGGAGACATGTGCAGCTTTCTTCATCCACACACA 120
QY 136 CCTGTGACATTTGTGAGACGAGAGACCGTAATAAAGTCTTCGTTATTAACACACAAA 195
DB 121 CCTGTGACATTTGTGAGACGAGAGACCGTAATAAAGTCTTCGTTATTAACACACAAA 180
QY 196 CCCCATTTGATTAAATGAATGATGATGATGATGATGATGATGATGATGATGATGAT 245
DB 181 CCCCATTTGATTAAATGAATGATGATGATGATGATGATGATGATGATGATGATGAT 230

XX XX Antifungal; biocontrol; binucleate; non-pathogenic fungus;
KW strain identification; classification; internal transcribed spacer;
KW ITS region; 5.8s region; ribosomal; ds.
XX
XX *Rhizoctonia* sp.
OS
XX W0200004779-A1.
PN
XX 03-FEB-2000.
PD
XX 23-JUN-1999; 99WO-GB02406.
PE
XX 24-JUL-1998; 98GB-0016265.
PR
XX (TECN-) INST TECNICO AGRONOMICO PROVINCIAL SA.
PA (RUFF/) RUFFLES G K.
PA
PI Rubio Susan V, Salazar Torres O, Julian Esquivias M;
PI Gonzales Garcia V, Gomez-Acebo Gullon E, Munoz Gomez R;
PI Lopez Corcoles H;
XX WPI: 2000-182492/16.
DR
XX
XX Protection of plants including tomato, pepper, lettuce, radish,
PT parsley, sugar beet, rape, and onions against pathogenic fungi, uses a
PT binucleate *Rhizoctonia* strain for biocontrol.
XX
XX Disclosure; Fig 1; 121pp; English.
XX
XX The invention relates to a novel method of protecting plants from
CC pathogenic fungi. The method comprises biocontrol of pathogenic fungi
CC via the use of a non-pathogenic, binucleate *Rhizoctonia* strain. The
CC binucleate *Rhizoctonia* is selected by molecular detection of certain
CC internal transcribed spacer (ITS)-5.8s ribosomal DNA sequences
CC (AA92445- AA92458), which vary between strains of these fungi. The
CC invention also encompasses a concentrate for use in plant protection
CC containing viable material from the binucleate *Rhizoctonia* strains of the
CC invention, and primers (AA92437-292444) for identifying these strains.
CC The strains of the invention are used as biocontrol agents for related
CC pathogenic fungi. Binucleate *Rhizoctonia* isolate Eab-F2 was tested for
CC its ability to protect tomato seedlings from the pathogenic *Rhizoctonia*
CC strain Me8.2. The *Rhizoctonia* strains were inoculated either
CC simultaneously or consecutively (the binucleate strain followed by the
CC pathogenic strain), and the protection effect indicated by the degree of
CC infected vegetal surface. The binucleate strain was found to provide
CC protection against the pathogenic strain when it had been allowed to
CC colonise the vegetal surface prior to pathogenic fungal infection (i.e.,
CC consecutive inoculation), whereas no protection was provided when both
CC strains were inoculated simultaneously. The method of the invention may
CC be used to protect a wide variety of plants from pathogenic fungal
CC infection. Plants that may be protected include vegetables, crops such as
CC oilseed rape, sugar beet and alfalfa, trees and ornamental plants. The
CC method is reliable and provides economical biocontrol of diseases caused
CC by *Rhizoctonia solani*. Sequences AA92445-292490 represent the ITS-5.8s
CC regions of ribosomal RNA-encoding DNA from a variety of *Rhizoctonia*
CC strains.
XX
SQ Sequence 408 BP; 109 A; 84 C; 91 G; 124 T; 0 other;
Query Match 70.6%; Score 173; DB 21; Length 408;
Best Local Similarity 90.1%; Pred. No. 2.9e-47;
Matches 219; Conservative 0; Mismatches 20; Indels 4; Gaps 3;
QY 5 AGGGGATTAAGAGTTCGTACAGAGTTCGTAAGTAACTCGGAGAGATCATTTATG 64
DB 13 AGAGGAGTAAGAGTTCGTACAGAGTTCGTAAGTAACTCGGAGAGATCATTTATG 72
QY 65 AATGAATATAGAGTTCGTTGCTGCTCCT--CCGAGAGATGTGACAGCTTTCTTT 122
DB 73 AATGAATATAGAGTTCGTTGCTGCTCCTTTCTTCTTCTTCTTCTTCTTCTT 132
QY 123 TCATCCACACACCTGTGACATTTGTGAGACGAGAGACCGTAATAAAGTCTTCGTTAT 182

ID	AA292466 standard; DNA; 411 BP.
XX	
AC	AA292466;
XX	
DT	05-JUN-2000 (first entry)
XX	
DE	Rhizoctonia sp. isolate AGBB ribosomal DNA, ITS1-5.8s region.
XX	
XX	Antifungal; biocontrol; binucleate; non-pathogenic fungus;
KW	strain identification; classification; internal transcribed spacer;
KW	ITS region; 5.8s region; ribosomal; ds.
XX	
XX	
OS	Rhizoctonia sp.
PN	WO200004779-A1.
PD	03-FEB-2000.
XX	
PF	23-JUL-1999; 99WO-GB02406.
XX	
PR	24-JUL-1998; 98GB-0016265.
XX	
XX	
IA	(TECN-) INST TECNICO AGRONOMICO PROVINCIAL SA.
PA	(RUFFN) RUFFLES G K.
PI	Rubio Susan V, Salazar Torres O, Julian Esquivias M;
PI	Gonzales Garcia V, Gomez-Acebo Gullon E, Munoz Gomez R;
XX	Lopez Corcoles H;
DR	WPI; 2000-182492/16.
XX	
PT	Protection of plants including tomato, pepper, lettuce, radish,
PT	parsley, sugar beet, rape, and onions against pathogenic fungi,
PT	binucleate Rhizoctonia strain for biocontrol -
XX	
PS	Disclosure: Fig 1; 121pp; English.
XX	
CC	The invention relates to a novel method of protecting plants from
CC	pathogenic fungi. The method comprises biocontrol of pathogenic fungi
CC	via the use of a non-pathogenic, binucleate Rhizoctonia strain. The
CC	binucleate Rhizoctonia is selected by molecular detection of certain
CC	internal transcribed spacer (ITS)-5.8s ribosomal DNA sequences
CC	(AA292445-AA292458), which vary between strains of these fungi. The
CC	invention also encompasses a concentrate for use in plant protection
CC	containing viable material from the binucleate Rhizoctonia strains of the
CC	invention, and primers (AA292437-292444) for identifying these strains.
CC	The strains of the invention are used as biocontrol agents for related
CC	pathogenic fungi. Binucleate Rhizoctonia isolate Fab-F2 was tested for
CC	its ability to protect tomato seedlings from the pathogenic Rhizoctonia
CC	strain Me8.2. The Rhizoctonia strains were inoculated either
CC	simultaneously or consecutively (the binucleate stain followed by the
CC	pathogenic strain), and the protection effect indicated by the degree of
CC	infected vegetal surface. The binucleate strain was found to provide
CC	protection against the pathogenic strain when it had been allowed to
CC	colonise the vegetal surface prior to pathogenic fungal infection (i.e.,
CC	consecutive inoculation), whereas no protection was provided when both
CC	strains were inoculated simultaneously. The method of the invention may
CC	be used to protect a wide variety of plants from pathogenic fungal
CC	infection. Plants that may be protected include vegetables, crops such as
CC	oilseed rape, sugar beet and alfalfa, trees and ornamental plants. The
CC	method is reliable and provides economical biocontrol of diseases caused
CC	by Rhizoctonia solani. Sequences AA292445-292490 represent the ITS-5.8s
CC	regions of ribosomal RNA-encoding DNA from a variety of Rhizoctonia
XX	strains.
XX	
SO	Sequence 411 BP; 112 A; 90 C; 89 G; 120 T; 0 other;
XX	
Query Match	57.5%; Score 140.8; DB 21; Length 411;
Best Local Similarity	79.6%; Pred. No. 1.4e-36;
Matches 191; Conservative	0; Mismatches 47; Indels 2; Gaps 2

Db	15	AGGGAAGCTAAAGTCGTAAAGAGTTTCCGTAGTGAACCTGGGGAAGATCATTTTG	74
Oy	65	AATGAATATAGAGTTGGTTGCTGCGTGCCT-CCTCCGGAGCATGTGACAGCTTTCTCT-T	122
Db	75	AATGAAGTTAAGAGTCGTGCTGCGTGGCTCTTTTGGAGCATGTGACAGCTTTCTCTAT	134
Oy	123	TCATCCACACACACCTGTGCACTGTGTGACAGCGAGGACCCGTAAGAAAGTCGTCCGTAT	182
Db	135	TCATCCACACACACCTGTGCACTGTGTGACAGCGAGGACCCGTAAGAAAGTCGTCCGTAT	194
Oy	183	TAAACACACAAACCCCATTTGTATTTTAAATGATGTAAATGTATGATGTAAACCATCATTTAA	242
Db	195	AAATCATATATCAAAACATCATTTAATGTAGACATGTATGATGTATGATGTATGATGTATGAT	254
RESULT 15			
AAZ92464			
ID	AAZ92464	standard; DNA; 410 BP.	
XX	AAZ92464;		
XX	05-JUN-2000	(first entry)	
XX	Rhizoctonia sp.	isolate AGP ribosomal DNA, ITS1-5.8s region.	
XX	Antifungal; biocontrol; binucleate; non-pathogenic fungus;		
XX	strain identification; classification; internal transcribed spacer;		
XX	ITS region; 5.8s region; ribosomal; ds.		
XX	Rhizoctonia sp.		
XX	WO200004779-A1.		
XX	03-FEB-2000.		
XX	23-JUL-1999;	99WO-GB02406.	
XX	24-JUL-1998;	98GB-0016265.	
XX	(TECN-) INST TECNICO AGRONOMICO PROVINCIAL SA.		
XX	(RUFE/) RUFELES G K.		
XX	Rubio Susan V, Salazar Torres O, Julian Esquivias M;		
XX	Gonzalez Garcia V, Gomez-Acedo Gullon E, Munoz Gomez R;		
XX	Lopez Corcoles H;		
XX	WPI; 2000-182492/16.		
XX	Protection of plants including tomato, pepper, lettuce, radish,		
XX	parsley, sugar beet, rape, and onions against pathogenic fungi, uses a		
XX	binucleate Rhizoctonia strain for biocontrol -		
XX	Disclosure: Fig 1; 121pp; English.		

CC strains were inoculated simultaneously. The method of the invention may
 CC be used to protect a wide variety of plants from pathogenic fungal
 CC infection. Plants that may be protected include vegetables, crops such as
 CC oilseed rape, sugar beet and alfalfa, trees and ornamental plants. The
 CC method is reliable and provides economical biocontrol of diseases caused
 CC by Rhizoctonia solani. Sequences AN292459-292490 represent the ITS-5.8s
 CC regions of ribosomal RNA-encoding DNA from a variety of Rhizoctonia
 CC strains.

XX Sequence 410 BP; 112 A; 87 C; 91 G; 120 T; 0 other;

Query Match 54.5%; Score 133.6; DB 21; Length 410;
 Best Local Similarity 80.2%; Pred. No. 3.4e-34;
 Matches 194; Conservative 0; Mismatches 44; Indels 4; Gaps 3;

QY 5 AGGGGATATAAAGTCGTAAACAAGTTCCGTAGTGAACCTCGGAGAGATCATTTATG 64
 Db 12 AGAGGAAGTAAAGTCGTAAACAAGTTCCGTAGTGAACCTCGGAGAGATCATTTATG 71
 QY 65 AATGATA--TAGAGTTGGTTGCGCTGGCT--CCTCCGGAGCATGTGCACGCTTCTCT 121
 Db 72 AATGAACACTTGGAGTCGCTTTCGCTGGCTGCTTTGGCAGCATGTGCACGCTTCTCT 131
 QY 122 -TTTCATCCACACACACCTGTGCACTGTGAGAGGAGACCGTAAAAAGCTTCCGCTCT 180
 Db 132 ATTCAATCCACACACACCTGTGCACTGTGAGAGGAGCGGAAAAAGCCTTCAGTCTG 191
 QY 181 ATTAAACACACAAACCCCATTTGTAATTAATGATGTAATGATTAACGATCATTA 240
 Db 192 CTAAATTCAATTAACAACATTTAATGACTGAATGTACTGATGTAAACGATCATTA 251
 QY 241 AA 242
 Db 252 AA 253

Search completed: March 2, 2003, 08:04:54
 Job time : 132 secs

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OM nucleic - nucleic search, using SW model

Run on: March 2, 2003, 08:02:53 ; Search time 52 Seconds
(without alignments)
1444.919 Million cell updates/sec

Title: US-09-744-502-20
Perfect score: 245
Sequence: 1 ttagaggggaataaaagtc.....tgaacgcatcataaact 245

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*

1: /cgn2_6/pdata/1/lna/5A.COMB.seq:*
2: /cgn2_6/pdata/1/lna/5B.COMB.seq:*
3: /cgn2_6/pdata/1/lna/6A.COMB.seq:*
4: /cgn2_6/pdata/1/lna/6B.COMB.seq:*
5: /cgn2_6/pdata/1/lna/PCTUS.COMB.seq:*
6: /cgn2_6/pdata/1/lna/Backfilest1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52.4	21.4	870	2	US-08-778-912A-4
2	52.4	21.4	870	4	US-09-541-941B-4
3	52.4	21.4	874	2	US-08-778-912A-1
4	52.4	21.4	874	4	US-09-541-941B-2
5	52.4	21.4	875	2	US-08-778-912A-2
6	52.4	21.4	875	2	US-08-778-912A-3
7	52.4	21.4	875	2	US-08-778-912A-5
8	52.4	21.4	875	2	US-08-778-912A-7
9	52.4	21.4	875	4	US-09-541-941B-1
10	52.4	21.4	875	4	US-09-541-941B-3
11	52.4	21.4	875	4	US-09-541-941B-5
12	52.4	21.4	875	4	US-09-541-941B-7
13	52.4	21.4	876	2	US-08-778-912A-6
14	52.4	21.4	876	4	US-09-541-941B-6
15	52.2	21.3	1788	2	US-08-867-820A-1
16	52	20.6	568	4	US-08-986-727-5
17	50.4	20.6	344	4	US-09-488-295-1
18	48.2	19.7	772	4	US-08-998-416-492
19	47.2	19.3	581	1	US-08-652-127C-6
20	47.2	19.3	583	1	US-08-652-127C-8
21	47.2	19.3	594	1	US-08-652-127C-5
22	47.2	19.3	594	4	US-09-645-073-1
23	46	18.8	617	3	US-08-986-727-2
24	46	18.8	1750	3	US-08-949-770-1
25	45.6	18.6	605	3	US-08-986-727-1
26	44.6	18.2	608	3	US-08-986-727-3
27	44.6	18.2	611	3	US-08-986-727-4

28	43	17.6	899	1	US-08-416-831B-1	Sequence 1, Appli
29	40.6	16.6	370	4	US-09-450-656-2	Sequence 2, Appli
30	40.4	16.5	917	4	US-09-541-941B-18	Sequence 18, Appli
31	40.4	16.5	918	4	US-09-541-941B-16	Sequence 16, Appli
32	40.4	16.5	918	4	US-09-541-941B-17	Sequence 17, Appli
33	40.4	16.5	918	4	US-09-541-941B-27	Sequence 27, Appli
34	40.2	16.4	312	1	US-08-400-580A-2	Sequence 2, Appli
35	39.2	16.0	267	1	US-08-400-580A-1	Sequence 1, Appli
36	39.2	16.0	267	1	US-08-400-580A-3	Sequence 3, Appli
37	38.8	15.8	898	4	US-09-541-941B-22	Sequence 22, Appli
38	38.8	15.8	898	4	US-09-541-941B-23	Sequence 23, Appli
39	38.8	15.8	898	4	US-09-541-941B-24	Sequence 24, Appli
40	38.8	15.8	898	4	US-09-541-941B-25	Sequence 25, Appli
41	38.8	15.8	918	4	US-09-541-941B-19	Sequence 19, Appli
42	37.2	15.2	815	4	US-09-541-941B-20	Sequence 20, Appli
43	37.2	15.2	904	4	US-09-541-941B-21	Sequence 21, Appli
44	35.2	14.4	4256	1	US-08-505-509-31	Sequence 31, Appli
45	35.2	14.4	4256	2	US-08-491-690A-31	Sequence 31, Appli

ALIGNMENTS

RESULT 1
US-08-778-912A-4/c
; Sequence 4, Application US/08778912A
; Patent No. 5876977
; GENERAL INFORMATION:
; APPLICANT: Wang, Jun
; APPLICANT: Ngan, F N
; APPLICANT: But, P P
; APPLICANT: Shaw, P C
; TITLE OF INVENTION: POLYMERASE CHAIN REACTION-RESTRICTION FRAGMENT
; TITLE OF INVENTION: TRADITIONAL CHINESE MEDICINES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/778,912A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Chan, Albert Wai-Kit
; REGISTRATION NUMBER: 36,479
; REFERENCE/DOCKET NUMBER: 52188
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 278 0400
; TELEFAX: 212 391 0526
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 870 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-778-912A-4
; Query Match 21.4%; Score 52.4; DB 2; Length 870;
; Best local similarity 90.3%; Pred. No. 1.1e-08;
; Matches 56; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
; 5 AGGGGAATMAAAGTCGTACAGGTTCCGTAGGTGACCGCGAAGCATCATTTATTG 64

Db 762 AGAGGAGAGAGAGTCTGTAACAAGGTTCCGTAGGTGAACCTGCGGAAGGATCATTTGCG 703

Qy 65 AA 66

Db 702 AA 701

RESULT 2

US-09-541-941B-4/C
; Sequence 4, Application US/09541941B
; Patent No. 6309840
; GENERAL INFORMATION:
; APPLICANT: Wang, Jun
; APPLICANT: Shaw, Pang Chui
; APPLICANT: Paul, Pul-Hay
; APPLICANT: Ngan, But/and Fai Ngor Karenda Ngan
; TITLE OF INVENTION: POLYMERASE CHAIN REACTION - RESTRICTION FRAGMENT LENGTH POLYMORPH
; FILE REFERENCE: 2913/52188-2A
; CURRENT APPLICATION NUMBER: US/09/541,941B
; CURRENT FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 870
; TYPE: DNA
; ORGANISM: P. Ginseng
US-09-541-941B-4

Query Match 21.4%; Score 52.4; DB 4; Length 870;
Best Local Similarity 90.3%; Pred. No. 1.1e-08;
Matches 56; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 5 AGGGGAATATAAAAGTCTGTAACAAGGTTCCGTAGGTGAACCTGCGGAAGGATCATTTATG 64

Db 762 AGAGGAGAGAGAGTCTGTAACAAGGTTCCGTAGGTGAACCTGCGGAAGGATCATTTGCG 703

Qy 65 AA 66

Db 702 AA 701

RESULT 3

US-08-778-912A-1/C
; Sequence 1, Application US/08778912A
; Patent No. 5876977
; GENERAL INFORMATION:
; APPLICANT: Wang, Jun
; APPLICANT: Ngan, F N
; APPLICANT: But, P P
; APPLICANT: Shaw, P C
; TITLE OF INVENTION: POLYMERASE CHAIN REACTION-RESTRICTION FRAGMENT
; TITLE OF INVENTION: LENGTH POLYMORPHISM TEST FOR THE AUTHENTICATION OF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/778,912A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

NAME: Chan, Albert Wai-Kit
REGISTRATION NUMBER: 36,479
REFERENCE/DOCKET NUMBER: 52188
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 278 0400
TELEFAX: 212 391 0526
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 874 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-778-912A-1

Query Match

21.4%; Score 52.4; DB 2; Length 874;
Best Local Similarity 90.3%; Pred. No. 1.1e-08;
Matches 56; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 5 AGGGGAATATAAAAGTCTGTAACAAGGTTCCGTAGGTGAACCTGCGGAAGGATCATTTATG 64

Db 760 AGAGGAGAGAGAGTCTGTAACAAGGTTCCGTAGGTGAACCTGCGGAAGGATCATTTGCG 701

Qy 65 AA 66

Db 700 AA 699

RESULT 4

US-09-541-941B-2/C
; Sequence 2, Application US/09541941B
; Patent No. 6309840
; GENERAL INFORMATION:
; APPLICANT: Wang, Jun
; APPLICANT: Shaw, Pang Chui
; APPLICANT: Paul, Pul-Hay
; APPLICANT: Ngan, But/and Fai Ngor Karenda Ngan
; TITLE OF INVENTION: POLYMERASE CHAIN REACTION - RESTRICTION FRAGMENT LENGTH POLYMO
; FILE REFERENCE: 2913/52188-2A
; CURRENT APPLICATION NUMBER: US/09/541,941B
; CURRENT FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 874
; TYPE: DNA
; ORGANISM: P. Ginseng
US-09-541-941B-2

Query Match 21.4%; Score 52.4; DB 4; Length 874;
Best Local Similarity 90.3%; Pred. No. 1.1e-08;
Matches 56; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 5 AGGGGAATATAAAAGTCTGTAACAAGGTTCCGTAGGTGAACCTGCGGAAGGATCATTTATG 64

Db 760 AGAGGAGAGAGAGTCTGTAACAAGGTTCCGTAGGTGAACCTGCGGAAGGATCATTTGCG 701

Qy 65 AA 66

Db 700 AA 699

RESULT 5

US-08-778-912A-2/C
; Sequence 2, Application US/08778912A
; Patent No. 5876977
; GENERAL INFORMATION:
; APPLICANT: Wang, Jun
; APPLICANT: Ngan, F N
; APPLICANT: But, P P
; APPLICANT: Shaw, P C
; TITLE OF INVENTION: POLYMERASE CHAIN REACTION-RESTRICTION FRAGMENT

;; TITLE OF INVENTION: LENGTH POLYMORPHISM TEST FOR THE AUTHENTICATION OF
;; TITLE OF INVENTION: TRADITIONAL CHINESE MEDICINES
;; NUMBER OF SEQUENCES: 15
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Cooper & Dunham LLP
;; STREET: 1185 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10036
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/778,912A
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Chan, Albert Wai-Kit
;; REGISTRATION NUMBER: 36,479
;; REFERENCE/DOCKET NUMBER: 52188
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212 278 0400
;; TELEFAX: 212 391 0526
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 875 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
;; US-08-778-912A-2

Query Match 21.4%; Score 52.4; DB 2; Length 875;
Best Local Similarity 90.3%; Pred. No. 1.1e-08;
Matches 56; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 AGGGATAAAAGTCGTAAACAGGTTCCGTAGTGAGTAACCTGGGAGGATCATTTATG 64
DB 761 AGAGGAGAGGAGAGTCTGTACCAAGGTTCCGTAGTGAGTAACCTGGGAGGATCATTTGCG 702

QY 65 AA 66
DB 701 AA 700

RESULT 6
US-08-778-912A-3/c
; Sequence 3, Application US/08778912A
; Patent No. 5876977
; GENERAL INFORMATION:
; APPLICANT: Wang, Jun
; APPLICANT: Ngan, F N
; APPLICANT: But, P P
; APPLICANT: Shaw, P C
; TITLE OF INVENTION: POLYMERASE CHAIN REACTION-RESTRICTION FRAGMENT
; TITLE OF INVENTION: LENGTH POLYMORPHISM TEST FOR THE AUTHENTICATION OF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/778,912A
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Chan, Albert Wai-Kit
;; REGISTRATION NUMBER: 36,479
;; REFERENCE/DOCKET NUMBER: 52188
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212 278 0400
;; TELEFAX: 212 391 0526
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 875 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
;; US-08-778-912A-3

Query Match 21.4%; Score 52.4; DB 2; Length 875;
Best Local Similarity 90.3%; Pred. No. 1.1e-08;
Matches 56; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 AGGGATAAAAGTCGTAAACAGGTTCCGTAGTGAGTAACCTGGGAGGATCATTTATG 64
DB 761 AGAGGAGAGGAGAGTCTGTACCAAGGTTCCGTAGTGAGTAACCTGGGAGGATCATTTGCG 702

QY 65 AA 66
DB 701 AA 700

RESULT 7
US-08-778-912A-5/c
; Sequence 5, Application US/08778912A
; Patent No. 5876977
; GENERAL INFORMATION:
; APPLICANT: Wang, Jun
; APPLICANT: Ngan, F N
; APPLICANT: But, P P
; APPLICANT: Shaw, P C
; TITLE OF INVENTION: POLYMERASE CHAIN REACTION-RESTRICTION FRAGMENT
; TITLE OF INVENTION: LENGTH POLYMORPHISM TEST FOR THE AUTHENTICATION OF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/778,912A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Chan, Albert Wai-Kit
; REGISTRATION NUMBER: 36,479
; REFERENCE/DOCKET NUMBER: 52188
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 278 0400
; TELEFAX: 212 391 0526
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 875 base pairs
; TYPE: nucleic acid

RESULT 11
US-09-541-941B-5/c
; Sequence 5, Application US/09541941B
; Patent No. 6309840
; GENERAL INFORMATION:
; APPLICANT: Wang, Jun
; APPLICANT: Shaw, Pang Chui
; APPLICANT: Ngan, But/Hay
; TITLE OF INVENTION: POLYMERASE CHAIN REACTION - RESTRICTION FRAGMENT LENGTH POLYMORPHISM
; FILE REFERENCE: 2913/52188-ZA
; CURRENT APPLICATION NUMBER: US/09/541,941B
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 875
; TYPE: DNA
; ORGANISM: P. Japonicus
US-09-541-941B-5

Query Match
Best Local Similarity 90.3%; Pred. No. 1.1e-08;
Matches 56; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 AGGGGAATATAAGTCTGTAACAAGTTTCCTAGTGAACCTCGGGAAGATCATTTATTG 64
DB 761 AGAGGAAGAGAGAGTCTGTAACAAGTTTCCTAGTGAACCTCGGGAAGATCATTTGCG 702
QY 65 AA 66
DB 701 AA 700

RESULT 12
US-09-541-941B-7/c
; Sequence 7, Application US/09541941B
; Patent No. 6309840
; GENERAL INFORMATION:
; APPLICANT: Wang, Jun
; APPLICANT: Shaw, Pang Chui
; APPLICANT: Ngan, But/Hay
; TITLE OF INVENTION: POLYMERASE CHAIN REACTION - RESTRICTION FRAGMENT LENGTH POLYMORPHISM
; FILE REFERENCE: 2913/52188-ZA
; CURRENT APPLICATION NUMBER: US/09/541,941B
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 875
; TYPE: DNA
; ORGANISM: P. Trifolium
US-09-541-941B-7

Query Match
Best Local Similarity 90.3%; Pred. No. 1.1e-08;
Matches 56; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 AGGGGAATATAAGTCTGTAACAAGTTTCCTAGTGAACCTCGGGAAGATCATTTATTG 64
DB 762 AGAGGAAGAGAGTCTGTAACAAGTTTCCTAGTGAACCTCGGGAAGATCATTTGTCG 703
QY 65 AA 66
DB 702 AA 701

RESULT 13
US-08-778-912A-6/c
; Sequence 6, Application US/08778912A

; Patent No. 5876977
; GENERAL INFORMATION:
; APPLICANT: Wang, Jun
; APPLICANT: Ngan, F N
; APPLICANT: But, P P
; APPLICANT: Shaw, P C
; TITLE OF INVENTION: POLYMERASE CHAIN REACTION-RESTRICTION FRAGMENT LENGTH POLYMORPHISM TEST FOR THE AUTHENTICATION OF TRADITIONAL CHINESE MEDICINES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/778,912A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Chan, Albert Wai-Kit
; REGISTRATION NUMBER: 36,479
; REFERENCE/DOCKET NUMBER: 52188
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 278 0400
; TELEFAX: 212 391 0526
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 876 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-778-912A-6

Query Match
Best Local Similarity 90.3%; Pred. No. 1.1e-08;
Matches 56; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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DB 762 AGAGGAAGAGAGTCTGTAACAAGTTTCCTAGTGAACCTCGGGAAGATCATTTGCG 703
QY 65 AA 66
DB 702 AA 701

RESULT 14
US-09-541-941B-6/c
; Sequence 6, Application US/09541941B
; Patent No. 6309840
; GENERAL INFORMATION:
; APPLICANT: Wang, Jun
; APPLICANT: Shaw, Pang Chui
; APPLICANT: Ngan, But/Hay
; TITLE OF INVENTION: POLYMERASE CHAIN REACTION - RESTRICTION FRAGMENT LENGTH POLYMORPHISM
; FILE REFERENCE: 2913/52188-ZA
; CURRENT APPLICATION NUMBER: US/09/541,941B
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 876

TYPE: DNA
ORGANISM: P. No. 6309840oginseng
US-09-541-941B-6

Query Match 21.4%; Score 52.4; DB 4; Length 876;
Best Local Similarity 90.3%; Pred. No. 1.1e-08;
Matches 56; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 AGGGGAATAAAAGTCGTACAGAGTTCCGTAGCTGAACCTGCGGAGAGATCATTTATG 64
Db 762 AGAGGAAGAGAGAGAGTCGTACAGAGTTCCGTAGCTGAACCTGCGGAGAGATCATTTATG 703
QY 65 AA 66
Db 702 AA 701

RESULT 15

US-08-867-820A-1
Sequence 1, Application US/08867820A
Patent No. 5891685
GENERAL INFORMATION:
APPLICANT: YAMAGISHI Masahiro
APPLICANT: TAKAI Yukie
APPLICANT: MIKAWA Takashi
APPLICANT: HARA Mari
APPLICANT: UEDA Makoto
APPLICANT: OHARA Akiko
TITLE OF INVENTION: METHOD FOR PRODUCING ESTER OF (S) - HALOGENATED - HYDROXYBUTY
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESSES:
ADDRESSEE: WENDEROTH, LIND & PONACK, L.L.P.
STREET: 2033 K Street, N.W., Suite 800
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867, 820A
FILING DATE: June 3, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: 1416/OP574US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1788 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Candida albicans
STRAIN: MUCCL29800
US-08-867-820A-1

Query Match 21.3%; Score 52.2; DB 2; Length 1788;
Best Local Similarity 94.7%; Pred. No. 1.7e-08;
Matches 54; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 AGGGGAATAAAAGTCGTACAGAGTTCCGTAGCTGAACCTGCGGAGAGATCATTTA 61
Db 1732 AGAGGAAGTAAAGTCGTACAGAGTTCCGTAGCTGAACCTGCGGAGAGATCATTTA 1788

Search completed: March 2, 2003, 11:17:00
Job time : 58 secs

GenCore version 5.1.4-p5.4578
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OM nucleic - nucleic search, using sw model

Run on: March 2, 2003, 08:04:59 ; Search time 69 seconds
(without alignments)
2214.299 Million cell updates/sec

Title: US-09-744-502-20

Perfect score: 245

Sequence: 1 tttagaggggaataaaagtc.....tgaacgacatcataaact 245

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 460893 seqs, 311809382 residues

Total number of hits satisfying chosen parameters: 921786

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications_NA.*
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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
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13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	57	23.3	253	9	US-09-768-020-59
2	56.2	22.9	42999	9	US-09-799-462A-17
3	56.2	22.9	42999	9	US-10-125-767-17
4	56.2	22.9	42999	9	US-09-836-911A-17
5	52.4	21.4	870	10	US-09-897-231-4
6	52.4	21.4	874	10	US-09-897-231-2
7	52.4	21.4	875	10	US-09-897-231-1
8	52.4	21.4	875	10	US-09-897-231-3
9	52.4	21.4	875	10	US-09-897-231-5
10	52.4	21.4	875	10	US-09-897-231-7
11	52.4	21.4	876	10	US-09-897-231-6
12	52.2	21.3	1969	10	US-09-880-107-2231
13	52.2	21.3	22118	9	US-09-799-462A-16
14	52.2	21.3	22118	9	US-10-125-767-16
15	52.2	21.3	22118	9	US-09-815-981-5
16	52.2	21.3	22118	9	US-09-836-911A-16
17	51.4	21.0	4240	9	US-09-938-842A-2248
18	48	19.6	1808	10	US-09-771-935B-17
19	40.4	16.5	917	10	US-09-897-231-18

20	40.4	16.5	918	10	US-09-897-231-16	Sequence 16, Appl
21	40.4	16.5	918	10	US-09-897-231-17	Sequence 17, Appl
22	40.4	16.5	1193	10	US-09-897-231-27	Sequence 27, Appl
23	40.4	16.5	640681	10	US-09-790-988-1	Sequence 1, Appl1
24	38.8	15.8	898	10	US-09-897-231-22	Sequence 22, Appl
25	38.8	15.8	898	10	US-09-897-231-23	Sequence 24, Appl
26	38.8	15.8	898	10	US-09-897-231-24	Sequence 25, Appl
27	38.8	15.8	898	10	US-09-897-231-25	Sequence 19, Appl
28	38.8	15.8	898	10	US-09-897-231-19	Sequence 20, Appl
29	37.2	15.2	815	10	US-09-897-231-20	Sequence 21, Appl
30	37.2	15.2	904	10	US-09-897-231-21	Sequence 1, Appl1
31	37.2	15.2	32998	9	US-10-027-806-1	Sequence 1, Appl1
32	37.2	15.2	32998	9	US-10-034-623-1	Sequence 2, Appl1
33	37.2	15.2	42432	9	US-10-027-806-2	Sequence 2, Appl1
34	37.2	15.2	42432	9	US-10-034-623-2	Sequence 137, App
35	36.2	14.8	140	10	US-09-925-299-137	Sequence 4, Appl1
36	35.4	14.4	641	9	US-09-766-173C-4	Sequence 79, Appl
37	35	14.3	446	9	US-10-074-246-79	Sequence 78, Appl
38	35	14.3	600	9	US-10-074-246-78	Sequence 77, Appl
39	35	14.3	653	9	US-10-074-246-77	Sequence 80, Appl
40	35	14.3	660	9	US-10-074-246-80	Sequence 3, Appl1
41	35	14.3	1467	10	US-09-726-774-3	Sequence 7, Appl1
42	35	14.3	1541	10	US-09-027-439-7	Sequence 2, Appl1
43	35	14.3	1541	10	US-09-726-774-2	Sequence 5, Appl1
44	35	14.3	1544	10	US-09-726-774-5	Sequence 89, Appl
45	35	14.3	1549	10	US-09-912-020-89	

ALIGNMENTS

RESULT 1
US-09-768-020-59
; Sequence 59, Application US/09768020
; Patent No. US2002017447A1
; GENERAL INFORMATION:
; APPLICANT: Greenspan, Ralph J.
; APPLICANT: Edelman, Gerald M.
; TITLE OF INVENTION: Method For Functional Mapping of An
; TITLE OF INVENTION: Alzheimer's Disease Gene Network and For Identifying
; FILE REFERENCE: P-NI 4577
; CURRENT FILING DATE: 2001-01-23
; PRIOR FILING DATE: 2000-01-24
; PRIOR APPLICATION NUMBER: US 09/490,243
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 253
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-768-020-59

Query Match 23.3%, Score 57; DB 9; Length 253;
Best Local Similarity 92.3%; Pred. No. 4.3e+09;
Matches 60; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 AGGGAATTAAGTCGTACACAGGTTTCCTAGTGAAGTGGGAGGATCTATTG 64
DB 137 AGAGGAATTAAGTCGTACACAGGTTTCCTAGTGAAGTGGGAGGATCTATTG 196

QY 65 AATGA 69
DB 197 TATTA 201

RESULT 2
US-09-799-462A-17
; Sequence 17, Application US/09799462A
; Patent No. US20020160970A1
; GENERAL INFORMATION:
; APPLICANT: Hadlaczky, Gyula

Slalay, Aladar
TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF
AND METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES
METHODS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McCauliffe
STREET: 4250 Executive Square, 7th Floor
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/799,462A
FILING DATE: 10-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/835,682
FILING DATE: 10-APR-1997
APPLICATION NUMBER: 08/695,191
FILING DATE: 07-AUG-1996
APPLICATION NUMBER: 08/682,080
FILING DATE: 15-JUL-1996
APPLICATION NUMBER: 08/629,822
FILING DATE: 10-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24601-402G
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858-450-8403
TELEFAX: 858-587-5360
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 42999 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-799-462A-17
Query Match 22.9%; Score 56.2; DB 9; Length 42999;
Best Local Similarity 63.9%; Pred. No. 6.7e-08;
Matches 85; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
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|||||
DB 5471 AGAGGAATAAAAGTCGTACAAAGTTCCGTAGGTGAACCTGCGGAAGATCATTTAAG 5530
|||||
QY 65 AATGAATATAGAGTTGTTGCTGCTCCGCGGAGCATGTCCACGCTTTCCTTTC 124
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DB 5531 GAGCCCGGAGGCGGAGCGCGCGCGCGCGCGCGCGCGCGCTTCCCTCCGACAC 5590
|||||
QY 125 ATCCACACACAC 137
|||||
DB 5591 CCACCCCGCCAC 5603

RESULT 3
US-10-125-767-17
Sequence 17, Application US/10125767
Patent No. US20020160410A1
GENERAL INFORMATION:

Applicant: Hadjaczky, Gyula
TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF AND
METHODS
FOR PREPARING ARTIFICIAL CHROMOSOMES
METHODS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McCauliffe LLP
STREET: 4350 La Jolla Village Drive, 7th Floor
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/125,767
FILING DATE: 17-Apr-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/724,693
FILING DATE: 28-NOV-2000
APPLICATION NUMBER: 08/835,682
FILING DATE: 10-APR-1997
APPLICATION NUMBER: 08/695,191
FILING DATE: 07-AUG-1996
APPLICATION NUMBER: 08/682,080
FILING DATE: 15-JUL-1996
APPLICATION NUMBER: 08/629,822
FILING DATE: 10-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24601-402J
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858-450-8403
TELEFAX: 858-587-5360
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 42999 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-125-767-17
Query Match 22.9%; Score 56.2; DB 9; Length 42999;
Best Local Similarity 63.9%; Pred. No. 6.7e-08;
Matches 85; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
QY 5 AGGGGAATAAAAGTCGTACAAAGTTCCGTAGGTGAACCTGCGGAAGATCATTTATG 64
|||||
DB 5471 AGAGGAATAAAAGTCGTACAAAGTTCCGTAGGTGAACCTGCGGAAGATCATTTAAG 5530
|||||
QY 65 AATGAATATAGAGTTGTTGCTGCTCCGCGGAGCATGTCCACGCTTTCCTTTC 124
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QY 125 ATCCACACACAC 137
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DB 5591 CCACCCCGCCAC 5603

RESULT 4
US-09-836-911A-17
Sequence 17, Application US/09836911A

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Publication No. US20030033617A1
GENERAL INFORMATION:
APPLICANT: Hadlaczky, Gyula
Szalay, Aladar
TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF
AND METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McCauliffe
STREET: 4350 La Jolla Village Drive, 6th Floor
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/836,911A
FILING DATE: 17-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/835,682
FILING DATE: 10-APR-1997
APPLICATION NUMBER: 08/695,191
FILING DATE: 07-AUG-1996
APPLICATION NUMBER: 08/682,080
FILING DATE: 15-JUL-1996
APPLICATION NUMBER: 08/629,822
FILING DATE: 10-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24601-4021
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858-450-8403
TELEFAX: 858-587-5360
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 42999 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-836-911A-17

Query Match          22.9%; Score 56.2; DB 9; Length 42999;
Best Local Similarity 63.9%; Pred. No. 6.7e-08;
Matches . 85; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 5 AGGGGAATAAAAGTGTAAACAAGTTTCGTAAGTGAACCTGCGAGAGATCATTTATTG 64
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Db 5471 AGAGGAAGTAAAGTCGTAAACAAGTTTCGTAAGTGAACCTGCGAGAGATCATTTAAACG 5530

QY 65 AATGATATATAGATTGGTGTCTGCTGCTCTCCGGAGACGATGTGACGCTTCTCTTC 124
  || ||| | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5531 GACGCCGAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTCCTCCGACAC 5590

QY 125 ATCCACACACAC 137
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Db 5591 CCACCCCCCACC 5603

RESULT 5
US-09-897-231-4/c
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Sequence 4, Application US/09897231
Patent No. US20020146705A1
GENERAL INFORMATION:
APPLICANT: Wang et al., Jun
TITLE OF INVENTION: POLYMERASE CHAIN REACTION - RESTRICTION FRAGMENT LENGTH POLYMO
TITLE OF INVENTION: FOR THE AUTHENTICATION OF TRADITIONAL CHINESE MEDICINES
FILE REFERENCE: 2913/52188-ZB
CURRENT APPLICATION NUMBER: US/09/897,231
CURRENT FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 870
TYPE: DNA
ORGANISM: P.Ginseng
US-09-897-231-4

Query Match          21.4%; Score 52.4; DB 10; Length 870;
Best Local Similarity 90.3%; Pred. No. 2.3e-07;
Matches 56; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 AGGGGAATAAAAGTGTAAACAAGTTTCGTAAGTGAACCTGCGAGAGATCATTTATTG 64
  || ||| | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 762 AGAGGAAGGAGAGTGTAAACAAGTTTCGTAAGTGAACCTGCGAGAGATCATTTGCG 703

QY 65 AA 66
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Db 702 AA 701

RESULT 6
US-09-897-231-2/c
Sequence 2, Application US/09897231
Patent No. US20020146705A1
GENERAL INFORMATION:
APPLICANT: Wang et al., Jun
TITLE OF INVENTION: POLYMERASE CHAIN REACTION - RESTRICTION FRAGMENT LENGTH POLYMO
TITLE OF INVENTION: FOR THE AUTHENTICATION OF TRADITIONAL CHINESE MEDICINES
FILE REFERENCE: 2913/52188-ZB
CURRENT APPLICATION NUMBER: US/09/897,231
CURRENT FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 874
TYPE: DNA
ORGANISM: P.Ginseng
US-09-897-231-2

Query Match          21.4%; Score 52.4; DB 10; Length 874;
Best Local Similarity 90.3%; Pred. No. 2.3e-07;
Matches 56; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 AGGGGAATAAAAGTGTAAACAAGTTTCGTAAGTGAACCTGCGAGAGATCATTTATTG 64
  || ||| | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 760 AGAGGAAGGAGAGTGTAAACAAGTTTCGTAAGTGAACCTGCGAGAGATCATTTGCG 701

QY 65 AA 66
  ||
Db 700 AA 699

RESULT 7
US-09-897-231-1/c
Sequence 1, Application US/09897231
Patent No. US20020146705A1
GENERAL INFORMATION:
APPLICANT: Wang et al., Jun
TITLE OF INVENTION: POLYMERASE CHAIN REACTION - RESTRICTION FRAGMENT LENGTH POLYMO
TITLE OF INVENTION: FOR THE AUTHENTICATION OF TRADITIONAL CHINESE MEDICINES
FILE REFERENCE: 2913/52188-ZB
CURRENT APPLICATION NUMBER: US/09/897,231
CURRENT FILING DATE: 2001-09-10
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NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 875
TYPE: DNA
ORGANISM: Quinquefolius
US-09-897-231-1

Query Match 21.4%; Score 52.4; DB 10; Length 875;
Best Local Similarity 90.3%; Pred. No. 2.3e-07;
Matches 56; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 AGGGGATTAAGTCTGTAACAGCTTCCGTAGCTGACCTGGCGAAGATCATTTATG 64
DB 761 AGAGGAAGAGAGAGTCTGTAACAGCTTCCGTAGCTGACCTGGCGAAGATCATTTGTCG 702

QY 65 AA 66
DB 701 AA 700

RESULT 8
US-09-897-231-3/c
Sequence 3, Application US/09897231
Patent No. US20020146705A1

GENERAL INFORMATION:
APPLICANT: Wang et al., Jun
TITLE OF INVENTION: POLYMERASE CHAIN REACTION - RESTRICTION FRAGMENT LENGTH POLYMO
FILE REFERENCE: 2913/52188-ZB
CURRENT APPLICATION NUMBER: US/09/897,231
CURRENT FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 875
TYPE: DNA
ORGANISM: P. Ginseng
US-09-897-231-3

Query Match 21.4%; Score 52.4; DB 10; Length 875;
Best Local Similarity 90.3%; Pred. No. 2.3e-07;
Matches 56; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 AGGGGATTAAGTCTGTAACAGCTTCCGTAGCTGACCTGGCGAAGATCATTTATG 64
DB 761 AGAGGAAGAGAGAGTCTGTAACAGCTTCCGTAGCTGACCTGGCGAAGATCATTTGTCG 702

QY 65 AA 66
DB 701 AA 700

RESULT 9
US-09-897-231-5/c
Sequence 5, Application US/09897231
Patent No. US20020146705A1

GENERAL INFORMATION:
APPLICANT: Wang et al., Jun
TITLE OF INVENTION: POLYMERASE CHAIN REACTION - RESTRICTION FRAGMENT LENGTH POLYMO
FILE REFERENCE: 2913/52188-ZB
CURRENT APPLICATION NUMBER: US/09/897,231
CURRENT FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5
LENGTH: 875
TYPE: DNA
ORGANISM: P. Japonicus
US-09-897-231-5

Query Match 21.4%; Score 52.4; DB 10; Length 875;

Best Local Similarity 90.3%; Pred. No. 2.3e-07;
Matches 56; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 AGGGGATTAAGTCTGTAACAGCTTCCGTAGCTGACCTGGCGAAGATCATTTATG 64
DB 761 AGAGGAAGAGAGAGTCTGTAACAGCTTCCGTAGCTGACCTGGCGAAGATCATTTGTCG 702

QY 65 AA 66
DB 701 AA 700

RESULT 10
US-09-897-231-7/c
Sequence 7, Application US/09897231
Patent No. US20020146705A1

GENERAL INFORMATION:
APPLICANT: Wang et al., Jun
TITLE OF INVENTION: POLYMERASE CHAIN REACTION - RESTRICTION FRAGMENT LENGTH POLYMO
FILE REFERENCE: 2913/52188-ZB
CURRENT APPLICATION NUMBER: US/09/897,231
CURRENT FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.0
SEQ ID NO 7
LENGTH: 875
TYPE: DNA
ORGANISM: P. trifolium
US-09-897-231-7

Query Match 21.4%; Score 52.4; DB 10; Length 875;
Best Local Similarity 90.3%; Pred. No. 2.3e-07;
Matches 56; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 AGGGGATTAAGTCTGTAACAGCTTCCGTAGCTGACCTGGCGAAGATCATTTATG 64
DB 762 AGAGGAAGAGAGAGTCTGTAACAGCTTCCGTAGCTGACCTGGCGAAGATCATTTGTCG 703

QY 65 AA 66
DB 702 AA 701

RESULT 11
US-09-897-231-6/c
Sequence 6, Application US/09897231
Patent No. US20020146705A1

GENERAL INFORMATION:
APPLICANT: Wang et al., Jun
TITLE OF INVENTION: POLYMERASE CHAIN REACTION - RESTRICTION FRAGMENT LENGTH POLYMO
FILE REFERENCE: 2913/52188-ZB
CURRENT APPLICATION NUMBER: US/09/897,231
CURRENT FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 876
TYPE: DNA
ORGANISM: P. No. US20020146705A1 Ginseng
US-09-897-231-6

Query Match 21.4%; Score 52.4; DB 10; Length 876;
Best Local Similarity 90.3%; Pred. No. 2.3e-07;
Matches 56; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 AGGGGATTAAGTCTGTAACAGCTTCCGTAGCTGACCTGGCGAAGATCATTTATG 64
DB 762 AGAGGAAGAGAGAGTCTGTAACAGCTTCCGTAGCTGACCTGGCGAAGATCATTTGTCG 703

QY 65 AA 66
DB 701 AA 700

Db 702 AA 701

RESULT 12
US-09-880-107-2231; Sequence 2231, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe

; APPLICANT: Gene Logic, Inc.

; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer

; FILE REFERENCE: 44921-5028-WO

; CURRENT APPLICATION NUMBER: US/09/880,107

; PRIOR FILING DATE: 2001-06-14

; PRIOR APPLICATION NUMBER: US 60/211,379

; PRIOR FILING DATE: 2000-06-14

; PRIOR APPLICATION NUMBER: US 60/237,054

; NUMBER OF SEQ ID NOS: 3950

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2231

; LENGTH: 1969

; TYPE: DNA

; ORGANISM: Homo sapiens

; OTHER INFORMATION: Genbank Accession No. US20020142981A1 M10098

; NAME/KEY: unsure

; LOCATION: (1)..(1969)

; OTHER INFORMATION: n = a or c or g or t

US-09-880-107-2231

Query Match 21.3%; Score 52.2; DB 10; Length 1969;

Best Local Similarity 94.7%; Pred. No. 3.7e-07;

Matches 54; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 13

US-09-799-462A-16

; Sequence 16, Application US/09799462A

; Patent No. US20020160970A1

; GENERAL INFORMATION:

; APPLICANT: Hadlaczky, Gyula

; APPLICANT: Szalay, Aladar

; TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF

; ADDRESS: Heller Ehtman White & Mcauliffe

; STREET: 4250 Executive Square, 7th Floor

; CITY: La Jolla

; STATE: CA

; COUNTRY: USA

; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/799,462A

; FILING DATE: 10-Sep-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/835,682

; FILING DATE: 10-Apr-1997

; APPLICATION NUMBER: 08/695,191

; FILING DATE: 07-AUG-1996

APPLICATION NUMBER: 08/682,080

FILING DATE: 15-JUL-1996

APPLICATION NUMBER: 08/629,822

FILING DATE: 10-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L

REGISTRATION NUMBER: 33,779

REFERENCE/DOCKET NUMBER: 24601-402G

TELECOMMUNICATION INFORMATION:

TELEPHONE: 858-450-8403

TELEFAX: 858-587-5360

TELEX: <unknown>

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 2218 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Genomic DNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: <unknown>

ORIGINAL SOURCE:

SEQUENCE DESCRIPTION: SEQ ID NO: 16:

US-09-799-462A-16

Query Match 21.3%; Score 52.2; DB 9; Length 2218;

Best Local Similarity 94.7%; Pred. No. 1e-06;

Matches 54; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 14

US-10-125-767-16

; Sequence 16, Application US/10125767

; Patent No. US20020160410A1

; GENERAL INFORMATION:

; APPLICANT: Hadlaczky, Gyula

; APPLICANT: Szalay, Aladar

; TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF AND

; ADDRESS: Heller Ehtman White & Mcauliffe LLP

; STREET: 4350 La Jolla Village Drive, 7th Floor

; CITY: San Diego

; STATE: CA

; COUNTRY: USA

; ZIP: 92122

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/125,767

; FILING DATE: 17-Apr-2002

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/724,693

; FILING DATE: 28-NOV-2000

; APPLICATION NUMBER: 08/835,682

; FILING DATE: 10-APR-1997

; APPLICATION NUMBER: 08/695,191

; FILING DATE: 07-AUG-1996

; APPLICATION NUMBER: 08/82,080

; FILING DATE: 15-JUL-1996

; APPLICATION NUMBER: 08/629,822

; FILING DATE: 10-APR-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Seidman, Stephanie L

GenCore version 5.1.4 p5_4578
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OM nucleic - nucleic search, using sw model

Run on: March 2, 2003, 07:55:23 ; Search time 1743 Seconds

(without alignments)
2276.474 Million cell updates/sec

Title: US-09-744-502-20

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Scoring table: IDENTITY_NUC
Gap 10.0, Gapext 1.0

Searched: 16154066 seqs, 809774376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

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1: em_estba: *
2: em_esthum: *
3: em_estin: *
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6: em_estpl: *
7: em_estro: *
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9: gb_est1: *
10: gb_est2: *
11: gb_hlc: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estfun: *
16: em_estom: *
17: gb_gss: *
18: em_gss_hum: *
19: em_gss_inv: *
20: em_gss_pln: *
21: em_gss_vrt: *
22: em_gss_fun: *
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25: em_gss_other: *
26: em_gss_pro: *
27: em_gss_rod: *

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	67.8	27.7	761	14	BU0383322
2	57.2	23.3	393	17	CI8A10
3	57.2	23.3	421	17	CI19H6
4	57.2	23.3	514	14	BP013583
5	57.2	23.3	544	10	AV953658
6	57.2	23.3	574	10	AV956116

Result No.	Score	Query Match	Length	DB ID	Description
7	57.2	23.3	598	17	CI2A11
8	57.2	23.3	602	10	AV966409
9	57.2	23.3	602	17	CI7G3
10	57.2	23.3	625	17	CI9G3
11	57.2	23.3	631	17	CI8E6
12	57.2	23.3	633	17	CI14B8
13	57.2	23.3	637	17	CI19C9
14	57.2	23.3	647	17	CI18E7
15	57.2	23.3	659	10	AV884174
16	57.2	23.3	673	14	BP017870
17	57.2	23.3	678	17	CI8B11
18	57.2	23.3	682	12	BE635943
19	57.2	23.3	695	9	AA141495
20	57.2	23.3	662	9	AA141460
21	57.2	23.3	875	17	CNS06YCH
22	57.2	23.3	882	17	CNS06XIS
23	57.2	23.3	968	17	CNS06XLP
24	57.2	23.3	1001	17	CNS06XW7
25	57.2	23.3	1002	17	CNS06YOX
26	57.2	23.3	1021	17	CNS06YON
27	57.2	23.3	1021	17	CNS06XYQ
28	57.2	23.3	1024	17	CNS06XWF
29	57.2	23.3	1026	17	CNS06YOG
30	56.8	23.2	339	17	CI19B10
31	56.6	23.1	902	17	CNS06XIR
32	56.6	23.1	953	17	CNS06YCT
33	56.4	23.0	316	17	AZ818673
34	56.4	23.0	341	17	AZ700886
35	56.4	23.0	345	17	AQ920611
36	56.4	23.0	350	17	AZ003429
37	56.4	23.0	356	17	AZ284060
38	56.4	23.0	500	13	BM195843
39	56.4	23.0	543	12	BE076758
40	56.4	23.0	559	17	AZ806266
41	56.4	23.0	587	13	BM198750
42	56.4	23.0	593	17	AZ361589
43	56.4	23.0	634	17	AZ988517
44	56.4	23.0	707	17	CI22H5
45	56.2	22.9	432	17	AZ917373

ALIGNMENTS

RESULT 1
LOCUS BU0383322
DEFINITION LIT0000228 Root-induced cDNA library from Laccaria bicolor Laccaria
ACCESSION BU0383322
VERSION BU0383322.1 GI:22473842
KEYWORDS EST.
SOURCE Laccaria bicolor.
ORGANISM Laccaria bicolor.
REFERENCE Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes; Agaricales; Tricholomataceae; Laccaria.
1 (bases 1 to 761)
Podila, G.K., Brand, J.R. and Hynes, M.J.
Root-induced cDNA library from Laccaria bicolor
Unpublished (2002).
CONTACT: Dr. G.K. Podila
Department of Biological Sciences
University of Alabama
Huntsville, AL 35899, USA
Tel: 256 824 6263
Fax: 256 824 6305
Email: podilagemall.nah.edu.

FEATURES

source
1..761
/organism="Laccaria bicolor"
/db_xref="taxon:29883"
/clone_id="Root-induced cDNA library from Laccaria bicolor"

/note="Laccaria bicolor in an interaction medium was exposed to Pinus resinosa roots for 6, 12, 24, 36, 48, 72 and 96 hours; the fungal tissue was then collected and frozen. Total mRNA was isolated from Laccaria tissue and pooled. This pooled mRNA was used to prepare a cDNA library. ESTs were randomly selected and sequenced to identify differentially expressed genes induced by root exudates using macroarray analysis."

BASE COUNT 168 a 167 c 192 g 225 t 9 others

Query Match 27.7%; Score 67.8; DB 14; Length 761;
Best Local Similarity 73.1%; Pred. No. 1.6e-10;
Matches 87; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

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OY 65 AATGAATATAGAGTTGTTGCTGCTGCTCCGCGGAGATGTCACGCTTTCCTTT 123
DB 533 AATAAAGCTGATGCTGCTGCTGCTTTCGAGACGATGCTGCTGCTGCTGCTT 591

RESULT 2
CIBA10 393 bp DNA linear GSS 03-DEC-2000
LACUS CIBA10
DEFINITION Ciona intestinalis genomic fragment, clone BAI0, genomic survey
ACCESSION AJ227478
VERSION AJ227478.1 GI:2951302
KEYWORDS GSS: genome survey sequence.
SOURCE Ciona intestinalis.
ORGANISM Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Clonidae; Clona.

REFERENCE 1 (bases 1 to 393)
AUTHORS Simmen,M.W., Lettgeb,S., Clark,V.H., Jones,S.J., and Bird,A.
TITLE Gene number in an invertebrate chordate, Ciona intestinalis
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (8), 4437-4440 (1998)
MEDLINE 98208558
PUBMED 9539755
REFERENCE 2 (bases 1 to 393)
AUTHORS Simmen,M.W., Lettgeb,S., Charlton,J., Jones,S.J., Harris,B.R., Clark,V.H., and Bird,A.
TITLE Nonmethylated transposable elements and methylated genes in a chordate genome
JOURNAL Science 283 (5405), 1164-1167 (1999)
MEDLINE 99148102
PUBMED 10024242

REFERENCE 3 (bases 1 to 393)
AUTHORS Simmen,M.W., and Bird,A.
TITLE Sequence analysis of transposable elements in the sea squirt, Ciona intestinalis
JOURNAL Mol. Biol. Evol. 17 (11), 1685-1694 (2000)
MEDLINE 20523971
PUBMED 11070056
REFERENCE 4 (bases 1 to 393)
AUTHORS Clark,V.H., Lettgeb,S., Charlton,J., Tweedie,S., Simmen,M.W., and Bird,A.P.
TITLE Direct Submission
COMMENT Submitted (28-FEB-1998) ICMB, University of Edinburgh, King's Buildings, Mayfield Rd, Edinburgh EH9 3JR, UK. E-mail contact: VCLARK@rsrv0.bio.ed.ac.uk
FEATURES Location/Qualifiers
source 1..393
/organism="Ciona intestinalis"
/db_xref="taxon:7719"
/clone="BA10"
/dev_stage="adult"

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Best Local Similarity 88.6%; Pred. No. 2.9e-07;
Matches 62; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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DB 2 AGAGGAAGTAAAGTCGTAAACAGGTTCCGTAGTGACCTGCGGAGATCATTTATTG 61
OY 65 AATGAATATA 74
DB 62 TATGAAGTA 71

RESULT 3
CIB19H6 421 bp DNA linear GSS 03-DEC-2000
LACUS CIB19H6
DEFINITION Ciona intestinalis genomic fragment, clone 19H6, genomic survey
ACCESSION AJ226748
VERSION AJ226748.1 GI:2950572
KEYWORDS GSS: genome survey sequence.
SOURCE Ciona intestinalis.
ORGANISM Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Clonidae; Clona.

REFERENCE 1 (bases 1 to 421)
AUTHORS Simmen,M.W., Lettgeb,S., Clark,V.H., Jones,S.J., and Bird,A.
TITLE Gene number in an invertebrate chordate, Ciona intestinalis
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (8), 4437-4440 (1998)
MEDLINE 98208558
PUBMED 9539755
REFERENCE 2 (bases 1 to 421)
AUTHORS Simmen,M.W., Lettgeb,S., Charlton,J., Jones,S.J., Harris,B.R., Clark,V.H., and Bird,A.
TITLE Nonmethylated transposable elements and methylated genes in a chordate genome
JOURNAL Science 283 (5405), 1164-1167 (1999)
MEDLINE 99148102
PUBMED 10024242

REFERENCE 3 (bases 1 to 421)
AUTHORS Simmen,M.W., and Bird,A.
TITLE Sequence analysis of transposable elements in the sea squirt, Ciona intestinalis
JOURNAL Mol. Biol. Evol. 17 (11), 1685-1694 (2000)
MEDLINE 20523971
PUBMED 11070056
REFERENCE 4 (bases 1 to 421)
AUTHORS Clark,V.H., Lettgeb,S., Charlton,J., Tweedie,S., Simmen,M.W., and Bird,A.P.
TITLE Direct Submission
COMMENT Submitted (28-FEB-1998) ICMB, University of Edinburgh, King's Buildings, Mayfield Rd, Edinburgh EH9 3JR, UK. E-mail contact: VCLARK@rsrv0.bio.ed.ac.uk
FEATURES Location/Qualifiers
source 1..421
/organism="Ciona intestinalis"
/db_xref="taxon:7719"
/clone="19H6"
/dev_stage="adult"

BASE COUNT 99 a 108 c 118 g 93 t 3 others

Query Match 23.3%; Score 57.2; DB 17; Length 421;
Best Local Similarity 88.6%; Pred. No. 3e-07;
Matches 62; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 5 AGGGAATATAAAAGTCGTAAACAGGTTCCGTAGTGACCTGCGGAGATCATTTATTG 64
DB 222 AGAGGAAGTAAAGTCGTAAACAGGTTCCGTAGTGACCTGCGGAGATCATTTATTG 281
OY 65 AATGAATATA 74

Db 282 TATGAAGCTA 291

RESULT 4

BP013583/c

LOCUS

DEFINITION

BP013583 514 bp mRNA linear EST 15-MAR-2002
BP013583 Nori Satoh unpublished cDNA library, young adult Ciona
intestinalis cDNA clone clad57113 5', mRNA sequence.

ACCESSION

BP013583

VERSION

BP013583.1 GI:19505060

KEYWORDS

EST.

SOURCE

Ciona intestinalis.

ORGANISM

Ciona intestinalis.

Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;

Phlebobranchia; Clonidae; Ciona.

1 (bases 1 to 514)

Satoh, N., Satou, Y., Kohara, Y. and Shin-I, T.

Expressed genes in Ciona intestinalis

Unpublished (2000)

Contact: Nori Satoh

Department of Zoology

Kyoto University

Sakyo-ku, Kyoto, Kyoto 606-8502, Japan

Tel: 81-75-753-4081

Fax: 81-75-705-1113

Email: satoh@ascidian.zool.kyoto-u.ac.jp.

Location/Qualifiers

1. 514

/organism="Ciona intestinalis"

/db_xref="taxon:7719"

/clone="clad57113"

/clone_lib="Nori Satoh unpublished cDNA library, young

adult"

/tissue_type="whole animal"

/dev_stage="young adult"

/note="Vector: pBluescript SK"

/note="Vector: pBluescript SK"

124 a 141 c 129 g 120 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 88.6%; Score 57.2; DB 14; Length 514;

Matches 62; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 5 AGGGGAATATAAAGTCGTACCAAGTTCCGTAGTGAACCTCGGAAGATCATTTATG 64

DB 72 AGAGGAAGTAAAGTCGTACCAAGTTCCGTAGTGAACCTCGGAAGATCATTTATG 13

QY 65 AATGAATATA 74

DB 12 TAAGAAAGTA 3

RESULT 5

AV953658/c

LOCUS

AV953658 544 bp mRNA linear EST 14-MAR-2002

AV953658 Nori Satoh unpublished cDNA library, young adult Ciona

intestinalis cDNA clone clad08a09 5', mRNA sequence.

AV953658

AV953658.1 GI:19441957

EST.

Ciona intestinalis.

Ciona intestinalis.

Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;

Phlebobranchia; Clonidae; Ciona.

1 (bases 1 to 544)

Satoh, N., Satou, Y., Kohara, Y. and Shin-I, T.

Expressed genes in Ciona intestinalis

Unpublished (2000)

Contact: Nori Satoh

Department of Zoology

Kyoto University

Sakyo-ku, Kyoto, Kyoto 606-8502, Japan

Tel: 81-75-753-4081

Fax: 81-75-705-1113

Email: satoh@ascidian.zool.kyoto-u.ac.jp.

Location/Qualifiers

1. 544

/organism="Ciona intestinalis"

/db_xref="taxon:7719"

/clone="clad08a09"

/clone_lib="Nori Satoh unpublished cDNA library, tailbud

embryo"

/tissue_type="whole animal"

/dev_stage="tailbud embryo"

/note="Vector: pBluescript SK"

/note="Vector: pBluescript SK"

113 a 187 c 143 g 129 t 2 others

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 88.6%; Score 57.2; DB 10; Length 574;

Matches 62; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 5 AGGGGAATATAAAGTCGTACCAAGTTCCGTAGTGAACCTCGGAAGATCATTTATG 64

DB 494 AGAGGAAGTAAAGTCGTACCAAGTTCCGTAGTGAACCTCGGAAGATCATTTATG 435

Tel: 81-75-753-4081
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FEATURES

Location/Qualifiers

1. 544

/organism="Ciona intestinalis"

/db_xref="taxon:7719"

/clone="clad08a09"

/clone_lib="Nori Satoh unpublished cDNA library, young

adult"

/tissue_type="whole animal"

/dev_stage="young adult"

/note="Vector: pBluescript SK"

/note="Vector: pBluescript SK"

123 a 157 c 142 g 122 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 88.6%; Score 57.2; DB 10; Length 544;

Matches 62; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 5 AGGGGAATATAAAGTCGTACCAAGTTCCGTAGTGAACCTCGGAAGATCATTTATG 64

DB 159 AGAGGAAGTAAAGTCGTACCAAGTTCCGTAGTGAACCTCGGAAGATCATTTATG 100

QY 65 AATGAATATA 74

DB 99 TAAGAAAGTA 90

RESULT 6

AV996116/c

LOCUS

AV996116 574 bp mRNA linear EST 15-MAR-2002

AV996116 Nori Satoh unpublished cDNA library, tailbud embryo Ciona

intestinalis cDNA clone clb43g13 5', mRNA sequence.

AV996116

AV996116.1 GI:19487450

EST.

Ciona intestinalis.

Ciona intestinalis.

Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;

Phlebobranchia; Clonidae; Ciona.

1 (bases 1 to 574)

Satoh, N., Satou, Y., Kohara, Y. and Shin-I, T.

Expressed genes in Ciona intestinalis

Unpublished (2000)

Contact: Nori Satoh

Department of Zoology

Kyoto University

Sakyo-ku, Kyoto, Kyoto 606-8502, Japan

Tel: 81-75-753-4081

Fax: 81-75-705-1113

Email: satoh@ascidian.zool.kyoto-u.ac.jp.

Location/Qualifiers

1. 574

/organism="Ciona intestinalis"

/db_xref="taxon:7719"

/clone="clb43g13"

/clone_lib="Nori Satoh unpublished cDNA library, tailbud

embryo"

/tissue_type="whole animal"

/dev_stage="tailbud embryo"

/note="Vector: pBluescript SK"

/note="Vector: pBluescript SK"

113 a 187 c 143 g 129 t 2 others

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 88.6%; Score 57.2; DB 10; Length 574;

Matches 62; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 5 AGGGGAATATAAAGTCGTACCAAGTTCCGTAGTGAACCTCGGAAGATCATTTATG 64

DB 494 AGAGGAAGTAAAGTCGTACCAAGTTCCGTAGTGAACCTCGGAAGATCATTTATG 435

OY 65 AATGATATA 74
 DB 434 TAAGAGGTA 425

RESULT 7
 C12A11 598 bp DNA 11near GSS 03-DEC-2000
 LOCUS Ciona intestinalis genomic fragment, clone 2A11, genomic survey
 DEFINITION sequence.

ACCESSION AJ227080.1 GI:2950906
 VERSION AJ227080.1
 KEYWORDS GSS: genome survey sequence.
 SOURCE Ciona intestinalis.
 ORGANISM Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Clonidae; Ciona.

REFERENCE 1 (bases 1 to 598)
 AUTHORS Simmen,M.W., Lettgeb,S., Clark,V.H., Jones,S.J., and Bird,A.
 TITLE Gene number in an invertebrate chordate, Ciona intestinalis
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (8), 4437-4440 (1998)
 MEDLINE 98208558
 PUBMED 9539755

REFERENCE 2 (bases 1 to 598)
 AUTHORS Simmen,M.W., Lettgeb,S., Charlton,J., Jones,S.J., Harris,B.R., Clark,V.H., and Bird,A.
 TITLE Nonmethylated transposable elements and methylated genes in a chordate genome
 JOURNAL Science 283 (5405), 1164-1167 (1999)
 MEDLINE 99148102
 PUBMED 10024242

REFERENCE 3 (bases 1 to 598)
 AUTHORS Simmen,M.W. and Bird,A.
 TITLE Sequence analysis of transposable elements in the sea squirt, Ciona intestinalis
 JOURNAL Mol. Biol. Evol. 17 (11), 1685-1694 (2000)
 MEDLINE 20523971
 PUBMED 11070056

REFERENCE 4 (bases 1 to 598)
 AUTHORS Clark,V.H., Lettgeb,S., Charlton,J., Tweedie,S., Simmen,M.W. and Bird,A.P.
 TITLE Direct Submission
 JOURNAL Submitted (28-FEB-1998) ICMB, University of Edinburgh, King's Buildings, Mayfield Rd, Edinburgh EH9 3JR, UK. E-mail contact: VCLAR@serv0.dio.ed.ac.uk
 COMMENT Location/Qualifiers
 FEATURES
 SOURCE 1..598
 /organism="Ciona intestinalis"
 /db_xref="taxon:7719"
 /clone="2A11"
 /dev_stage="adult"

BASE COUNT 135 a 150 c 178 g 134 t 1 others

ORIGIN

Query Match 23.3%; Score 57.2; DB 17; Length 598;
 Best Local Similarity 88.6%; Pred. No. 3.4e-07;
 Matches 62; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 5 AGGGAATTAAGTCTGTAACAGGTTTCCTAGGTGTAACCTCGGAGAGATCATTTATG 64
 DB 276 AGAGGAGTAAGTCTGTAACAGGTTTCCTAGGTGTAACCTCGGAGAGATCATTTATG 335

OY 65 AATGATATA 74
 DB 336 TATGAAGTA 345

RESULT 8
 AV966409/c 602 bp mRNA linear EST 14-MAR-2002
 LOCUS AV966409 Nori Satoh unpublished cDNA library, young adult Ciona
 DEFINITION intestinalis cDNA clone ctad16113 5', mRNA sequence.

ACCESSION AV966409
 VERSION AV966409.1 GI:19456105
 KEYWORDS EST.
 SOURCE Ciona intestinalis.
 ORGANISM Ciona intestinalis.
 Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Clonidae; Ciona.

REFERENCE 1 (bases 1 to 602)
 AUTHORS Satoh,N., Satou,Y., Kohara,Y. and Shin-I,T.
 TITLE Expressed genes in Ciona intestinalis
 JOURNAL Unpublished (2000)
 COMMENT Contact: Nori Satoh
 Department of Zoology
 Kyoto University
 Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
 Tel: 81-75-753-4081
 Fax: 81-75-705-1113
 Email: satoh@ascidian.zool.kyoto-u.ac.jp.

FEATURES
 source
 1..602
 /organism="Ciona intestinalis"
 /db_xref="taxon:7719"
 /clone="ctad16113"
 /clone_id="Nori Satoh unpublished cDNA library, young adult"
 /rissu_type="whole animal"
 /dev_stage="young adult"
 /note="Vector: pBluescript SK"

BASE COUNT 139 a 166 c 158 g 138 t 1 others

ORIGIN

Query Match 23.3%; Score 57.2; DB 10; Length 602;
 Best Local Similarity 88.6%; Pred. No. 3.4e-07;
 Matches 62; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 5 AGGGAATTAAGTCTGTAACAGGTTTCCTAGGTGTAACCTCGGAGAGATCATTTATG 64
 DB 165 AGAGGAGTAAGTCTGTAACAGGTTTCCTAGGTGTAACCTCGGAGAGATCATTTATG 106

OY 65 AATGATATA 74
 DB 105 TAAGAGGTA 96

RESULT 9
 C17G3 602 bp DNA linear GSS 03-DEC-2000
 LOCUS C17G3
 DEFINITION Ciona intestinalis genomic fragment, clone 7G3, genomic survey sequence.

ACCESSION AJ227462.1 GI:2951285
 VERSION AJ227462.1
 KEYWORDS GSS: genome survey sequence.
 SOURCE Ciona intestinalis.
 ORGANISM Ciona intestinalis.
 Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Clonidae; Ciona.

REFERENCE 1 (bases 1 to 602)
 AUTHORS Simmen,M.W., Lettgeb,S., Clark,V.H., Jones,S.J. and Bird,A.
 TITLE Gene number in an invertebrate chordate, Ciona intestinalis
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (8), 4437-4440 (1998)
 MEDLINE 98208558
 PUBMED 9539755

REFERENCE 2 (bases 1 to 602)
 AUTHORS Simmen,M.W., Lettgeb,S., Charlton,J., Jones,S.J., Harris,B.R., Clark,V.H. and Bird,A.
 TITLE Nonmethylated transposable elements and methylated genes in a chordate genome
 JOURNAL Science 283 (5405), 1164-1167 (1999)
 MEDLINE 99148102
 PUBMED 10024242

REFERENCE 3 (bases 1 to 602)
 AUTHORS Simmen,M.W. and Bird,A.
 TITLE Sequence analysis of transposable elements in the sea squirt, Ciona

COMMENT	VCLARK@serv0.bio.ed.ac.uk
FEATURES	Vector: pBluescript KS.
source	Location/Qualifiers 1. .625 /organism="Clona in

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/organism="Clona intestinalis"
/db_xref="taxon:7719"
/clone="963"
/dev_stage="adult"

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BASE COUNT	146 a	162 c	174 g	140 t	3 others
ORIGIN					

Query Match	23.38;	Score 57.2;	DB 17;	Length 625
Best Local Similarity	88.68;	Pred. No. 3	4e-07.	

Matches	Conservative	Mismatches	Indels	Gaps
62;	0;	8;	0;	0

D_b 430 AGAGGAGTAAAGTCGTACCAAGCTTTCCTAGCTGAACCTGCGGAGGATCATTAACG 489

Db 490 TATGAAGTGA 499

RESULT 11			
C18E6/c			
LOCUS	631 bp	DNA	
C18E6		linear	
DEFINITION	Clona intestinalis genomic fragment		GSS 03-DEC-2000

sequence.	
accession	AJ227516
version	AJ227516.1

ORGANISM	REFERENCE
<i>Clona intestinalis</i>	1 (bases 1 to 631)
<i>Eukaryota</i> ; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Clonidae; Clona.	1 (bases 1 to 631)
Slimmer, M.W., Leitegeb, S., Clark, V.H., Jones, S.J. and Bird, A.	Proc. Natl. Acad. Sci. U.S.A. 95 (8), 4437-4440 (1998)
GENE NUMBER	98208658
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 95 (8), 4437-4440 (1998)
MEDLINE	98208658
PUBLISHED	9539755
2 (bases 1 to 631)	

TITLE	Nonmethylated transposable elements and methylated genes in a choriolate genome
JOURNAL	Science 283 (5405), 1164-1167 (1999)
MEDLINE	99148102
PUBMED	10024242

AUTHORS	Simmen, M.W. and Bird, A.
TITLE	Sequence analysis of transposable elements in the <i>gus</i> control

Intestinals
Mol. Biol. Evol. 17 (11), 1685-1694 (2000)
MEDLINE 20523971
PUBMED 11070056
REFERENCE 4 (phases 1 to 631)

TITLE Bird, A.P.
DIRECT SUBMISSION Submitted (28-FEB-1998) ICMB, University of Edinburgh, King's Buildings, Mayfield Rd, Edinburgh EH9 3JR, UK. E-mail contact: VCLARK@serv.bio.ed.ac.uk
COMMENT Vector: null; no restriction enzyme sites.

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source
1. .631
/organism="Ciona im

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BASE COUNT
RIGIN
156 a 180 c 150 g 144 t 1 others
/dev_stage="adult"
/cd_alter="cdaxon:1/19"
/cd_alter="8E6"

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VERSION      AJ226664.1 GI:2950124
KEYWORDS     GSS: genome survey sequence.
SOURCE       Ciona intestinalis.
ORGANISM     Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
              Phlebobranchia; Cloniidae; Clona.
REFERENCE    1 (bases 1 to 647)
AUTHORS      Simmen,M.W., Leltgeb,S., Clark,V.H., Jones,S.J. and Bird,A.
TITLE        Gene number in an invertebrate chordate, Ciona intestinalis
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 95 (8), 4437-4440 (1998)
MEDLINE      98208558
PUBMED       9539755
REFERENCE    2 (bases 1 to 647)
AUTHORS      Simmen,M.W., Leltgeb,S., Charlton,J., Jones,S.J., Harris,B.R.,
TITLE        Clark,V.H. and Bird,A.
JOURNAL      Nonmethylated transposable elements and methylated genes in a
MEDLINE      chordate genome
PUBMED       science 283 (5405), 1164-1167 (1999)
REFERENCE    3 (bases 1 to 647)
AUTHORS      Simmen,M.W. and Bird,A.
TITLE        Sequence analysis of transposable elements in the sea squirt, Ciona
JOURNAL      Mol. Biol. Evol. 17 (11), 1685-1694 (2000)
MEDLINE      20523971
PUBMED       11070056
REFERENCE    4 (bases 1 to 647)
AUTHORS      Clark,V.H., Leltgeb,S., Charlton,J., Tweedie,S., Simmen,M.W. and
TITLE        Bird,A.P.
JOURNAL      Direct Submission
MEDLINE      Submitted (28-FEB-1998) ICMB, University of Edinburgh, King's
PUBMED       Buildings, Mayfield Rd, Edinburgh EH9 3JR, UK. E-mail contact:
REFERENCE    Vector: Bluescript SK.
AUTHORS      Location/Qualifiers
TITLE        1..647
JOURNAL      /organism="Ciona intestinalis"
MEDLINE      /db_xref="taxon:7719"
PUBMED       /clone="18E7"
REFERENCE    /dev_stage="adult"
AUTHORS      BASE COUNT      140 a      197 c      147 g      151 t      12 others
ORIGIN
Query Match      23.3%; Score 57.2; DB 17; Length 647;
Best Local Similarity 88.6%; Pred. No. 3.5e-07;
Matches 62; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY      5 AGGGGAATATAAAGTCGTACACAGGTTCCGTAGTGACCTGCGGAGGATCATATTG 64
        || ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      384 AGAGGAAGTAAAGTCGTACACAGGTTCCGTAGTGACCTGCGGAGGATCATATTG 64
QY      65 AATGAATATA 74
        || ||| ||
DB      324 TATGAAGTA 315

RESULT 15
LOCUS      AV884174
DEFINITION AV884174 Nori Satoh unpublished cDNA library, linear EST 08-NOV-2001
ACCESSION  AV884174
VERSION     AV884174
KEYWORDS   EST.
SOURCE     Ciona intestinalis.
ORGANISM  Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
              Phlebobranchia; Cloniidae; Clona.
REFERENCE  1 (bases 1 to 659)
AUTHORS    Satoh,N., Satou,Y., Kohara,Y. and Shin-I,T.
TITLE      Expressed genes in Ciona intestinalis
JOURNAL    Unpublished (2000)

```

```

COMMENT      Contact: Nori Satoh
              Department of Zoology
              Kyoto University
              Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
              Tel: 81-75-753-4081
              Fax: 81-75-705-1113
              Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES     Location/Qualifiers
              1..659
              /organism="Ciona intestinalis"
              /db_xref="taxon:7719"
              /clone="rc1b41k17"
              /clone_lib="Nori Satoh unpublished cDNA library, tailbud
              embryo"
              /tissue_type="whole animal"
              /dev_stage="tailbud embryo"
              /note="Vector: pBluescript SK"
BASE COUNT   147 a      194 c      167 g      150 t      1 others
ORIGIN
Query Match      23.3%; Score 57.2; DB 10; Length 659;
Best Local Similarity 88.6%; Pred. No. 3.5e-07;
Matches 62; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY      5 AGGGGAATATAAAGTCGTACACAGGTTCCGTAGTGACCTGCGGAGGATCATATTG 64
        || ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      205 AGAGGAAGTAAAGTCGTACACAGGTTCCGTAGTGACCTGCGGAGGATCATATTG 146
QY      65 AATGAATATA 74
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DB      145 TATGAAGTA 136

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Job time : 1750 secs

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